

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 1, 2005, 18:03:08 ; Search time 7593 Seconds
(without alignments)
10748.990 Million cell updates/sec

Title: US-10-030-294-1

Perfect score: 5676

Sequence: 1 cagctgttcaggatgtctg.....tttataattgttctcgt 5676

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27724519 seqs, 718965201 residues

Total number of hits satisfying chosen parameters: 55449038

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents_NA_New.*

1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
2: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq2.*
3: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
5: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq1.*
8: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq2.*
9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
10: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq10.*
11: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq11.*
12: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2.*
13: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq3.*
14: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq4.*
15: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq5.*
16: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq6.*
17: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq7.*
18: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq8.*
19: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq9.*
20: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq.*
21: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq2.*
22: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq3.*
23: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq4.*
24: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq5.*
25: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq6.*
26: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq7.*
27: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq8.*
28: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1987.4	35.0	255679	15	US-10-940-774A-17189, A Sequence 17189, A
2	632.6	11.1	633	7	US-09-925-065A-552295 Sequence 842014,
3	357.4	6.3	999	10	US-10-301-480C-344792 Sequence 344792,
4	357.4	6.3	999	17	US-10-301-480A-344792 Sequence 344792,
5	357.4	6.3	999	19	US-10-301-480B-344792 Sequence 344792,

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c      6      196.2      3.5      65793      13      US-10-703-817-3
      7      193.8      3.4      536      10      US-09-925-065A-552295
      8      193.8      3.4      536      10      US-10-301-480C-906314
      9      193.8      3.4      536      17      US-10-301-480A-906314
     10      193.8      3.4      536      18      US-10-301-480A-530245
     11      193.8      3.4      536      18      US-10-301-480A-1143654
     12      193.8      3.4      536      19      US-10-301-480B-906314
     13      193.8      3.4      80503      15      US-10-990-328A-94591
     14      192.2      3.4      536      7      US-09-925-065A-552294
     15      192.2      3.4      536      10      US-10-301-480C-906313
     16      192.2      3.4      536      17      US-10-301-480A-906313
     17      192.2      3.4      536      18      US-10-301-480A-530244
     18      192.2      3.4      536      18      US-10-301-480B-1143653
     19      192.2      3.4      536      19      US-10-301-480B-906313
     20      190.6      3.4      265038      15      US-10-940-774A-15779
     21      190.6      3.4      300351      15      US-10-990-328A-96853
     22      190.2      3.4      163565      15      US-10-990-328A-93556
     23      188.8      3.3      874      10      US-10-301-480C-259257
     24      188.8      3.3      874      17      US-10-301-480A-259257
     25      188.8      3.3      874      19      US-10-301-480B-259257
     26      187.6      3.3      739      10      US-10-301-480C-259258
     27      187.6      3.3      739      17      US-10-301-480A-259258
     28      187.6      3.3      739      19      US-10-301-480B-259258
     29      187      3.3      997      10      US-10-301-480C-256336
     30      187      3.3      997      17      US-10-301-480A-256336
     31      187      3.3      997      19      US-10-301-480B-256336
     32      186.8      3.3      991      10      US-10-301-480C-283512
     33      186.8      3.3      991      17      US-10-301-480A-283512
     34      186.8      3.3      991      19      US-10-301-480B-283512
     35      186.8      3.3      992      10      US-10-301-480C-283513
     36      186.8      3.3      992      17      US-10-301-480A-283513
     37      186.8      3.3      992      19      US-10-301-480B-283513
     38      186.6      3.3      652661      15      US-10-990-328A-97235
     39      186.4      3.3      601      15      US-10-940-774A-142852
     40      186      3.3      585      10      US-10-301-480C-597588
     41      186      3.3      585      17      US-10-301-480A-597588
     42      186      3.3      585      18      US-10-301-480-221519
     43      186      3.3      585      18      US-10-301-480-834928
     44      186      3.3      585      19      US-10-301-480B-597588
     45      186      3.3      587      7      US-09-925-065A-123687

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ALIGNMENTS

RESULT 1

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US-10-940-774A-17189
; Sequence 17189, Application US/10940774A
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/10/940,774A
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17189
; LENGTH: 255679
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) ..(255679)
; OTHER INFORMATION: n = A,T,C or G
US-10-940-774A-17189

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US-10-940-774A-17189

Query Match		35.0%; Score 1987.4; DB 15; Length 255679;
Best Local Similarity		99.9%; Pred. No. 1.8e-254;
Matches 1999; Conservative		0; Mismatches 1; Indels 1; Gaps 1;
Qy	3676	TATCCCTGGAGTTAAATTTAAATATTTAGAGAGTTCTTCCCTCATTTCTTAGAGAGCTC 3735
Db	1	TATCCCTGGAGTTAAATTTAAATATTTAGAGAGTTCTTCCCTCATTTCTTAGAGAGCTC 60
Qy	3736	GAATTTGTAATATCAGAGCTAGAGGAACTAGGGCTCGCACTCCAAAGTGTGGTCCA 3795
Db	61	GAATTTGTAATATCAGAGCTAGAGGAACTAGGGCTCGCACTCCAAAGTGTGGTCCA 120
Qy	3796	AGAACAGCAGCATCAAGTAACCTGGGAACGTGTAGAAATGCAAGTCTTAGGCTCAC 3855
Db	121	AGAACAGCAGCATCAAGTAACCTGGGAACGTGTAGAAATGCAAGTCTTAGGCTCAC 180
Qy	3856	CCAGACCTACTGAAACAGAAATCTGCATTAAACAAGATTTCTAGTGCCTCACGGGCACAT 3915
Db	181	CCAGACCTACTGAAACAGAAATCTGCATTAAACAAGATTTCTAGTGCCTCACGGGCACAT 240
Qy	3916	TAAACTTTGAGAGCTCTGCCTAGAAATCTTCACTCCACCTTTTCATTATTAATGGAATC 3975
Db	241	TAAACTTTGAGAGCTCTGCCTAGAAATCTTCACTCCACCTTTTCATTATTAATGGAATC 300
Qy	3976	ACTTGGGCTGTGTACAGGAAATTTGATTTTAAATTTTCAAGACCTTCTTATTTAGTTC 4035
Db	301	ACTT-GGCTGTGGTACAGGAAATTTGATTTTAAATTTTCAAGACCTTCTTATTTAGTTC 359
Qy	4036	ATCTATATTTCTTAATAGCAGGAAAGCAAACTCTTTAACTGCAATTTAAACAATCT 4095
Db	360	ATCTATATTTCTTAATAGCAGGAAAGCAAACTCTTTAACTGCAATTTAAACAATCT 419
Qy	4096	ATAATTAATTAAGTAAAGCAATCTTCCCTTTAAAGTTTTCATTTGTGGCAAGCTGTTT 4155
Db	420	ATAATTAATTAAGTAAAGCAATCTTCCCTTTAAAGTTTTCATTTGTGGCAAGCTGTTT 479
Qy	4156	GATTTGGCTGGGCTCAGGCGGCTGTTTGTGAATTTTCAAAATTCACAGATGTTAGCG 4215
Db	480	GATTTGGCTGGGCTCAGGCGGCTGTTTGTGAATTTTCAAAATTCACAGATGTTAGCG 539
Qy	4216	CTCTCGGCTAAGTAAAGGAAGAGAACTCAAGTTTAAATAGCTTCTCCCTTCCATCCT 4275
Db	540	CTCTCGGCTAAGTAAAGGAAGAGAACTCAAGTTTAAATAGCTTCTCCCTTCCATCCT 599
Qy	4276	GGCTGAAGCAACAAATAAAATATTTTATGAACAATTTTGGAGTTAGTACTTACAG 4335
Db	600	GGCTGAAGCAACAAATAAAATATTTTATGAACAATTTTGGAGTTAGTACTTACAG 659
Qy	4336	GGAAATGTCAAAATTTCTGAAAGGCTTTAGATTGTCTCAAACTTTGACATCTACTGA 4395
Db	660	GGAAATGTCAAAATTTCTGAAAGGCTTTAGATTGTCTCAAACTTTGACATCTACTGA 719
Qy	4396	TGTCACTTATTTACAGGTGTCTGTGACATAGGGGGTGAAGGAAGATGTGAATCTACC 4455
Db	720	TGTCACTTATTTACAGGTGTCTGTGACATAGGGGGTGAAGGAAGATGTGAATCTACC 779
Qy	4456	ATGTTAGTGAACGTTTATGATACACAGAGTGGTTTTTTTCCCTGTTGGAGTCTATCCTA 4515
Db	780	ATGTTAGTGAACGTTTATGATACACAGAGTGGTTTTTTTCCCTGTTGGAGTCTATCCTA 839
Qy	4516	ACTGAGCTTCTGAATCATATTTCAATTTCCAAATTCACAAACAGGATAGTTTGA 4575
Db	840	ACTGAGCTTCTGAATCATATTTCAATTTCCAAATTCACAAACAGGATAGTTTGA 899
Qy	4576	CAGCCCATTTACAGAAAGGAATAAATTTTGTGTGTAGACTTTTCCCTGATTTACACT 4635
Db	900	CAGCCCATTTACAGAAAGGAATAAATTTTGTGTGTAGACTTTTCCCTGATTTACACT 959
Qy	4636	GATTTGGGAATATATGAACAATTTTATGGTTTCTTTTGAAGTAGGTCAAGTCAAGCAA 4695
Db	960	GATTTGGGAATATATGAACAATTTTATGGTTTCTTTTGAAGTAGGTCAAGTCAAGCAA 1019
Qy	4696	AACCAAAACAGCAAAACCTGTAAACATATAAGATAGAGTGGAGCGGACTGAGAGATTA 4755

Db	1020	AACCAAAACAGCAAAACCTGTAAAGATTAAGATAGAGTGGAGCCGACTGAGAGATTA 1079
Qy	4756	AAATAAACTAGAATATTTTATTAACAGGCAATTTGAAATAATTTGTGCATTCAGAAATA 4815
Db	1080	AAATAAACTAGAATATTTTATTAACAGGCAATTTGAAATAATTTGTGCATTCAGAAATA 1139
Qy	4816	TTCTCAATTAATATATATTTTCCAAATTTTAAATATCTTTAAGAAAAATTTACTATATATG 4875
Db	1140	TTCTCAATTAATATATATTTTCCAAATTTTAAATATCTTTAAGAAAAATTTACTATATATG 1199
Qy	4876	TAAGTACATGTGCATGTGTTTGGAGTAGGATATTTAACTCAATAAAGGTTATTTTCTTTT 4935
Db	1200	TAAGTACATGTGCATGTGTTTGGAGTAGGATATTTAACTCAATAAAGGTTATTTTCTTTT 1259
Qy	4936	ATTCCGGTCAGGCAAAAGCTTCTAAGGGGATGTGAAGGGATATCTCTTTCTTTAGCTGA 4995
Db	1260	ATTCCGGTCAGGCAAAAGCTTCTAAGGGGATGTGAAGGGATATCTCTTTCTTTAGCTGA 1319
Qy	4996	GAGGAAGAGTGAGTTCTAAGTTAAATTAATCAAGGAATTTCCCTGTCTTTTGTCTATTGA 5055
Db	1320	GAGGAAGAGTGAGTTCTAAGTTAAATTAATCAAGGAATTTCCCTGTCTTTTGTCTATTGA 1379
Qy	5056	GATTTGACCAACAACAGCGGTTGGCTGAAAGGGGAACTGAAAGGCGGGAGGGAGGAA 5115
Db	1380	GATTTGACCAACAACAGCGGTTGGCTGAAAGGGGAACTGAAAGGCGGGAGGGAGGAA 1439
Qy	5116	ATAGATGAAAAAACAACAACAAACTTCCCTAAGAGAGCTCTACAAAACATTTTAGC 5175
Db	1440	ATAGATGAAAAAACAACAACAAACTTCCCTAAGAGAGCTCTACAAAACATTTTAGC 1499
Qy	5176	CCCAGAAATAGTCACAGAAATCTCAATCAAAACAGTATCCAGATCAAGGAAGTGTGA 5235
Db	1500	CCCAGAAATAGTCACAGAAATCTCAATCAAAACAGTATCCAGATCAAGGAAGTGTGA 1559
Qy	5236	TGTAGCTGGAGCAGGCTGGACACTCATCAGCTCAGTTTCAAGTTACAAAAGTCCAGGCT 5295
Db	1560	TGTAGCTGGAGCAGGCTGGACACTCATCAGCTCAGTTTCAAGTTACAAAAGTCCAGGCT 1619
Qy	5296	GAAATTAACCTCTGATGCCATTTATGCGAGATCCAAATCAGCAGAGATCAGAAAGTTCA 5355
Db	1620	GAAATTAACCTCTGATGCCATTTATGCGAGATCCAAATCAGCAGAGATCAGAAAGTTCA 1679
Qy	5356	GAGATGCTCCAGCTCCAAATTTGCCAACACAGTGTGGCTACTATAGTCAAGGACTCT 5415
Db	1680	GAGATGCTCCAGCTCCAAATTTGCCAACACAGTGTGGCTACTATAGTCAAGGACTCT 1739
Qy	5416	GAAGCCGTGAGAGAGGGGAGAAACAACAGTAGAGAGGATGCCAGCTGGTAAAGATCGA 5475
Db	1740	GAAGCCGTGAGAGAGGGGAGAAACAACAGTAGAGAGGATGCCAGCTGGTAAAGATCGA 1799
Qy	5476	GTGTTTATGAAGTTTATGTCATTTGATGAATCTCATTTGGCTTAAATCAAGAAAACGCTCC 5535
Db	1800	GTGTTTATGAAGTTTATGTCATTTGATGAATCTCATTTGGCTTAAATCAAGAAAACGCTCC 1859
Qy	5536	CCTCTTTGCAATATGATGAAGGAGAGAGTGTCTTAACTTTCTATGCTCATAGCATTT 5595
Db	1860	CCTCTTTGCAATATGATGAAGGAGAGAGTGTCTTAACTTTCTATGCTCATAGCATTT 1919
Qy	5596	GACCTATTTGCTTTTAGCTCCCGCTTTATCTATATATACAGGATATTTGTGTATA 5655
Db	1920	GACCTATTTGCTTTTAGCTCCCGCTTTATCTATATATACAGGATATTTGTGTATA 1979
Qy	5656	TTTTATATAATTTGTTCTCCGT 5676
Db	1980	TTTTATATAATTTGTTCTCCGT 2000

RESULT 2
US-09-925-065A-842014
; Sequence 842014, Application US/09925065A
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.

;; TITLE OF INVENTION: Identification and Mapping of Single
;; FILE REFERENCE: 108827.135
;; CURRENT APPLICATION NUMBER: US/09/925,065A
;; PRIOR FILING DATE: 2001-08-08
;; PRIOR APPLICATION NUMBER: US 60/243,096
;; PRIOR FILING DATE: 2000-10-24
;; PRIOR APPLICATION NUMBER: US 60/252,147
;; PRIOR FILING DATE: 2000-11-20
;; PRIOR APPLICATION NUMBER: US 60/250,092
;; PRIOR FILING DATE: 2000-11-30
;; PRIOR APPLICATION NUMBER: US 60/261,766
;; PRIOR FILING DATE: 2001-01-16
;; PRIOR APPLICATION NUMBER: US 60/289,846
;; PRIOR FILING DATE: 2001-05-09
;; NUMBER OF SEQ ID NOS: 957086
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 842014
;; LENGTH: 633
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-925-065A-842014

Query Match 11.1%; Score 632.6; DB 7; Length 633;
Best Local Similarity 99.8%; Pred. No. 8.7e-75;
Matches 632; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 4064 AGCCAACTCTTTAACTGCAATTAACAAATCTATAATTAATAGTAAAGCAATCTTCCCT 4123
Db 1 AGCCAACTCTTTAACTGCAATTAACAAATCTATAATTAATAGTAAAGCAATCTTCCCT 60
Qy 4124 TTAAGTTTAACTTTGTGGAGCAAGCTGTTGATTTGGCTGGGGCTCAGCGCGGCTGT 4183
Db 61 TTAAGTTTAACTTTGTGGAGCAAGCTGTTGATTTGGCTGGGGCTCAGCGCGGCTGT 120
Qy 4184 TTGTGAATTTACAAATTCACAGATGTTAGCGGCTCTGGGCTAGTAAGGAAGAGATG 4243
Db 121 TTGTGAATTTACAAATTCACAGATGTTAGCGGCTCTGGGCTAGTAAGGAAGAGATG 180
Qy 4244 TCAAGTTTAAATAGCTTCTCCCTTCCATCTGGCTGAAGCAACAAATAAATAATTTTAA 4303
Db 181 TCAAGTTTAAATAGCTTCTCCCTTCCATCTGGCTGAAGCAACAAATAAATAATTTTAA 240
Qy 4304 TGAACACATTTTTCAGTTAGATTTTACTTACAGGGAATGTCAAAATTTCTCTGAAAGGGCT 4363
Db 241 TGAACACATTTTTCAGTTAGATTTTACTTACAGGGAATGTCAAAATTTCTCTGAAAGGGCT 300
Qy 4364 TTAGATTTGCTCAACAATTTGACATCTACTGATGTCACTTATTTACAGGTGTGTCCTGTG 4423
Db 301 TTAGATTTGCTCAACAATTTGACATCTACTGATGTCACTTATTTACAGGTGTGTCCTGTG 360
Qy 4424 ACTAGGGGGTGAAGGAAGATGTCAACTCACATGTTAGTGACCGTTAGATACACAGAT 4483
Db 361 ACTAGGGGGTGAAGGAAGATGTCAACTCACATGTTAGTGACCGTTAGATACACAGAT 420
Qy 4484 GGTTTTTTTTCCCTCTGTGGAGTCTATCTTAAGTCTGAGCTTCTGAATCATATTTTCATCA 4543
Db 421 GGTTTTTTTTCCCTCTGTGGAGTCTATCTTAAGTCTGAGCTTCTGAATCATATTTTCATCA 480
Qy 4544 ATTTCGAATCCAAACCAAGGTAAGTTTACAGCCCATATTCAGAAAGGAATAAATTT 4603
Db 481 ATTTCGAATCCAAACCAAGGTAAGTTTACAGCCCATATTCAGAAAGGAATAAATTT 540
Qy 4604 ATTTGTGTGTAGACTTTTCTGATATTACACTGATTTGGGAATATATGAACAAATTTTATG 4663
Db 541 ATTTGTGTGTAGACTTTTCTGATATTACACTGATTTGGGAATATATGAACAAATTTTATG 600
Qy 4664 GTTTCCTTTTCAAGTAGTCAAGTCAAGCAAA 4696
Db 601 GTTTCCTTTTCAAGTAGTCAAGTCAAGCAAA 633

RESULT 3

US-10-301-480C-344792
;; Sequence 344792, Application US/10301480C
;; GENERAL INFORMATION:
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single
;; FILE REFERENCE: 108827-137
;; CURRENT APPLICATION NUMBER: US/10/301,480C
;; PRIOR FILING DATE: 2002-11-21
;; PRIOR APPLICATION NUMBER: US 10/215,598
;; PRIOR FILING DATE: 2002-08-09
;; PRIOR APPLICATION NUMBER: US 60/311,695
;; PRIOR FILING DATE: 2001-08-10
;; NUMBER OF SEQ ID NOS: 989478
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 344792
;; LENGTH: 999
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-301-480C-344792

Query Match 6.3%; Score 357.4; DB 10; Length 999;
Best Local Similarity 99.7%; Pred. No. 2.2e-36;
Matches 358; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAGCTGTTCAAGGGATGTCGAAAAGAGCCACCCACATTTGCTTCTGGACACTGGGTGT 60
Db 641 CAGCTGTTCAAGGGATGTCGAAAAGAGCCACCCACATTTGCTTCTGGACACTGGGTGT 700
Qy 61 GACTTTGGAGGGTATCAGGTTTGTCTGTTAAAGAACTGCCAACCTTCTCTGCCCAAT 120
Db 701 GACTTTGGAGGGTATCAGGTTTGTCTGTTAAAGAACTGCCAACCTTCTCTGCCCAAT 760
Qy 121 TGGCTCTGTTCCCTTGCATGCCCTCTTCTTGGGACACTCCCTTAAGGCATCTTCTTG 180
Db 761 TGGCTCTGTTCCCTTGCATGCCCTCTTCTTGGGACACTCCCTTAAGGCATCTTCTTG 820
Qy 181 ACATTAACTTAACATATAAATGTTTATTTGATGAATTTTCAAGTACCTGAAAGAGATGAG 240
Db 821 ACATTAACTTAACATATAAATGTTTATTTGATGAATTTTCAAGTACCTGAAAGAGATGAG 880
Qy 241 GTCAAAATCAGAAAGACACATGCTAAGTTGCAATGCATTTGCTTTTCAATTGAATTA 300
Db 881 GTCAAAATCAGAAAGACACATGCTAAGTTGCAATGCATTTGCTTTTCAATTGAATTA 940
Qy 301 AGTCATTGCAATACATTCAGTTTACTTAAAGTTCTAGGCCAGCTTTTACTCTTAATCGA 359
Db 941 AGTCATTGCAATACATTCAGTTTACTTAAAGTTCTAGGCCAGCTTTTACTCTTAATCGA 999

RESULT 4
US-10-301-480A-344792
;; Sequence 344792, Application US/10301480A
;; GENERAL INFORMATION:
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single
;; FILE REFERENCE: 108827-137
;; CURRENT APPLICATION NUMBER: US/10/301,480A
;; PRIOR FILING DATE: 2002-11-21
;; PRIOR APPLICATION NUMBER: US 10/215,598
;; PRIOR FILING DATE: 2002-08-09
;; PRIOR APPLICATION NUMBER: US 60/311,695
;; PRIOR FILING DATE: 2001-08-10
;; NUMBER OF SEQ ID NOS: 989478
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 344792
;; LENGTH: 999
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-301-480A-344792

Query Match 6.3%; Score 357.4; DB 17; Length 999;

Best Local Similarity 99.7%; Pred. No. 2.2e-38;
Matches 358; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAGCTGTTCAAGGATGTCGGAAGAGAGCCACCCACATGCTCTGGACACTGGGTGT 60
Db |||||
641 CAGCTGTTCAAGGATGTCGGAAGAGAGCCACCCACATGCTCTGGACACTGGGTGT 700
Qy 61 GACTTTGGAGGGTATCAGGTTTGTCTGTTAAGAAACTGCCAACCTCTTCTGCCCAAT 120
Db |||||
701 GACTTTGGAGGGTATCAGGTTTGTCTGTTAAGAAACTGCCAACCTCTTCTGCCCAAT 760
Qy 121 TGGCCTCTGTTCCCTGTCATGCCCTCTTCTCTGGGACACTCCCTTAAGGACATCTTTG 180
Db |||||
761 TGGCCTCTGTTCCCTGTCATGCCCTCTTCTCTGGGACACTCCCTTAAGGACATCTTTG 820
Qy 181 ACATTAACTTAACATATAAATGTTTATTTGATGAATTTTCAGTGACCTGAAGAGATGGAG 240
Db |||||
821 ACATTAACTTAACATATAAATGTTTATTTGATGAATTTTCAGTGACCTGAAGAGATGGAG 880
Qy 241 GTCAAAATCAGAAGACACATGGCTAAGGTTGCAATGCATCTGCTTTTTCATTGAATTA 300
Db |||||
881 GTCAAAATCAGAAGACACATGGCTAAGGTTGCAATGCATCTGCTTTTTCATTGAATTA 940
Qy 301 AGTCATTGGAATACCATTCAGTTTACTTAAGTTCTAGGCCAGCTTTTACTCCTTAATCGA 359
Db |||||
941 AGTCATTGGAATACCATTCAGTTTACTTAAGTTCTAGGCCAGCTTTTACTCCTTAATCGA 999

RESULT 5
US-10-301-480B-344792
; Sequence 344792, Application US/10301480B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 10827-137
; CURRENT APPLICATION NUMBER: US/10/301.480B
; PRIOR FILING DATE: 2002-11-21
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 989478
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 344792
; LENGTH: 999
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480B-344792

Query Match 6.3%; Score 357.4; DB 19; Length 999;
Best Local Similarity 99.7%; Pred. No. 2.2e-38;
Matches 358; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAGCTGTTCAAGGATGTCGGAAGAGAGCCACCCACATGCTCTGGACACTGGGTGT 60
Db 641 CAGCTGTTCAAGGATGTCGGAAGAGAGCCACCCACATGCTCTGGACACTGGGTGT 700
Qy 61 GACTTTGGAGGGTATCAGGTTTGTCTGTTAAGAAACTGCCAACCTCTTCTGCCCAAT 120
Db 701 GACTTTGGAGGGTATCAGGTTTGTCTGTTAAGAAACTGCCAACCTCTTCTGCCCAAT 760
Qy 121 TGGCCTCTGTTCCCTGTCATGCCCTCTTCTCTGGGACACTCCCTTAAGGACATCTTTG 180
Db 761 TGGCCTCTGTTCCCTGTCATGCCCTCTTCTCTGGGACACTCCCTTAAGGACATCTTTG 820
Qy 181 ACATTAACTTAACATATAAATGTTTATTTGATGAATTTTCAGTGACCTGAAGAGATGGAG 240
Db 821 ACATTAACTTAACATATAAATGTTTATTTGATGAATTTTCAGTGACCTGAAGAGATGGAG 880
Qy 241 GTCAAAATCAGAAGACACATGGCTAAGGTTGCAATGCATCTGCTTTTTCATTGAATTA 300
Db 881 GTCAAAATCAGAAGACACATGGCTAAGGTTGCAATGCATCTGCTTTTTCATTGAATTA 940

Qy 301 AGTCATTGGAATACCATTCAGTTTACTTAAGTTCTAGGCCAGCTTTTACTCCTTAATCGA 359
Db 941 AGTCATTGGAATACCATTCAGTTTACTTAAGTTCTAGGCCAGCTTTTACTCCTTAATCGA 999

RESULT 6
US-10-703-817-3/c
; Sequence 3, Application US/10703817
; GENERAL INFORMATION:
; APPLICANT: ROTH, RICHARD B.
; APPLICANT: NELSON, MATTHEW ROBERTS
; APPLICANT: KAMMERER, STEFAN M.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF MELANOMA AND TREATMENTS
; FILE REFERENCE: SEQ-4061-UT
; CURRENT APPLICATION NUMBER: US/10/703,817
; CURRENT FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: 60/489,703
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 60/424,475
; PRIOR FILING DATE: 2002-11-06
; NUMBER OF SEQ ID NOS: 255
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-703-817-3

Query Match 3.5%; Score 196.2; DB 13; Length 65793;
Best Local Similarity 70.0%; Pred. No. 2.7e-17;
Matches 278; Conservative 0; Mismatches 118; Indels 1; Gaps 1;

Qy 3262 CTTTTAAATTTTTTAAAAAATAGATGAGTGTGTGCTCATGCTGTAAATCCCAACACT 3321
Db 18059 CTATAAAGTTTTTTTACAGGAAAGCCAGGTGCGGTGCTCACACCTGTATCCAGCACT 18000
Qy 3322 TTGGGAAGCCGGTTCGGAGGATAGCTTTGAGTCCAGCAGTTTGAGACCACTGAGGGCAAC 3381
Db 17999 TTGGGAAGCTGAGGCAGGTGGAATGCTTGTAGCTCAGGAGTTTGAGACCAGCCTGGGCAAC 17940
Qy 3382 ACAGCAAGCCCCATATCTTAAAAAACAACAAAAAATACCTGGGTATGTTGTG 3441
Db 17939 ATGGCAAAAAATCTCTACATAAATAACAGAAAAAATAGCTGCGAGTTTGTGTGTG 17880
Qy 3442 CTCACCTGTAGTCCAAGCTACACAGGAAGCTGAGGCAAGAGGATCACTTGAGCCCCAGAG 3501
Db 17879 CACACCTGTGTCTCTGTTACTCAGGAGTCTGAGATGGAGGATGCTTGAGCCCCAGAG 17820
Qy 3502 GTTGAGGCTCAGTGATPCCATGAACGCGCTGTCTACACT-CAGTCTGGGTGACAGTGCAG 3560
Db 17819 ATTGAGGCTCAGTGAGCCCAAGATCATGCCACTGTACTCCAGCCTGGGCAACAGAGCAAG 17760
Qy 3561 AAGCTGTCTCAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3620
Db 17759 ACTCCATCTCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 17700
Qy 3621 ATTTTAAAAACACAAACACTAGAGATGTTTGGCAAT 3657
Db 17699 TATAATATATACACACACATATATATATATATATATATATATATATATATATATA 17663

RESULT 7
US-09-925-065A-552295
; Sequence 552295, Application US/09925065A
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A

; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 552295
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-552295

Query Match 3.4%; Score 193.8; DB 7; Length 536;
Best Local Similarity 70.9%; Pred. No. 1.1e-16;
Matches 270; Conservative 1; Mismatches 108; Indels 2; Gaps 1;

QY 3212 ATCATGACATACGTTTAAATGATATTATTTAAATAGTATTTAAATAGCTTAGGCTATAAACCTTTTAAATT 3271
Db 1 ATCTGTACAAAACATCTGATTTTCACCTTTTCAAAATCTTTAGGTAGTAAAGTTAAATCTTA 60
QY 3272 TTTTAAAAAATAGATGAGTGTGGCTCATCGCTGTAATCCCAACACTTTGGGAAGCC 3331
Db 61 AAGGTCAAAGATTGCTGGGTATGGTAGCTCACGCCCTGTATTCCAACTCTTAGGAGGCC 120
QY 3332 GGGTCGGGAGGATAGCTTGAGTCCAGAGTGTGAGACCAAGTCAAGTCCAGGCAACACAGCAAGAC 3391
Db 121 GAGCGGGCGTATCGCTTGAGCCAGGGGTTTGAGACCAAGTCAAGTCCAGGCAACACAGCAAGAC 180
QY 3392 CCATATCTAAAAAACAACAAACAAATTAATCTCTGGGTATGGTGTGCTCACCTGTA 3451
Db 181 CCATCTCTACAAAATAAAATATACA--ATAATGAGCTGGGCATGGTGGCAGCACCTGTG 238
QY 3452 GTCCAAGCTACACAGGAAGCTGAGGCGAGAGGATCACTTTGAGCCAGGAGTTTGAGGCTG 3511
Db 239 GTCCAGCTACTTTGGGAGGCTGAGGCGAGGATGCTTGAAGCCAGGAGTTTGGGCTG 298
QY 3512 CAGTGATCCATGAACCGCTGCTTACACTCAGTCTGGGTGACAGTGCAGAAAGCTGTCTCA 3571
Db 299 CAGTGAGCTGTGACTGTACTTCTGCACTCCACTGACAGTAAGACCCCTGTCTCA 358
QY 3572 AAAATAATAATAATAAAAA 3592
Db 359 AAAATAACAATAATAATAA 379

RESULT 8
US-10-301-480C-906314
; Sequence 906314, Application US/10301480C
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827-137
; CURRENT APPLICATION NUMBER: US/10/301,480C
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 989478
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 906314
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480C-906314

Query Match 3.4%; Score 193.8; DB 10; Length 536;
Best Local Similarity 70.9%; Pred. No. 1.1e-16;
Matches 270; Conservative 1; Mismatches 108; Indels 2; Gaps 1;

QY 3212 ATCATGACATACGTTTAAATGATATTATTTAAATAGCTTAGGCTATAAACCTTTTAAATT 3271
Db 1 ATCTGTACAAAACATCTGATTTTCACCTTTTCAAAATCTTTAGGTAGTAAAGTTAAATCTTA 60
QY 3272 TTTTAAAAAATAGATGAGTGTGGCTCATCGCTGTAATCCCAACACTTTGGGAAGCC 3331
Db 61 AAGGTCAAAGATTGCTGGGTATGGTAGCTCACGCCCTGTATTCCAACTCTTAGGAGGCC 120
QY 3332 GGGTCGGGAGGATAGCTTGAGTCCAGAGTGTGAGACCAAGTCAAGTCCAGGCAACACAGCAAGAC 3391
Db 121 GAGCGGGCGTATCGCTTGAGCCAGGGGTTTGAGACCAAGTCAAGTCCAGGCAACACAGCAAGAC 180
QY 3392 CCATATCTAAAAAACAACAAACAAATTAATCTCTGGGTATGGTGTGCTCACCTGTA 3451
Db 181 CCATCTCTACAAAATAAAATATACA--ATAATGAGCTGGGCATGGTGGCAGCACCTGTG 238
QY 3452 GTCCAAGCTACACAGGAAGCTGAGGCGAGAGGATCACTTTGAGCCAGGAGTTTGAGGCTG 3511
Db 239 GTCCAGCTACTTTGGGAGGCTGAGGCGAGGATGCTTGAAGCCAGGAGTTTGGGCTG 298
QY 3512 CAGTGATCCATGAACCGCTGCTTACACTCAGTCTGGGTGACAGTGCAGAAAGCTGTCTCA 3571
Db 299 CAGTGAGCTGTGACTGTACTTCTGCACTCCACTGACAGTAAGACCCCTGTCTCA 358
QY 3572 AAAATAATAATAATAAAAA 3592
Db 359 AAAATAACAATAATAATAA 379

RESULT 9
US-10-301-480A-906314
; Sequence 906314, Application US/10301480A
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827-137
; CURRENT APPLICATION NUMBER: US/10/301,480A
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 989478
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 906314
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480A-906314

Query Match 3.4%; Score 193.8; DB 17; Length 536;
Best Local Similarity 70.9%; Pred. No. 1.1e-16;
Matches 270; Conservative 1; Mismatches 108; Indels 2; Gaps 1;

QY 3212 ATCATGACATACGTTTAAATGATATTATTTAAATAGCTTAGGCTATAAACCTTTTAAATT 3271
Db 1 ATCTGTACAAAACATCTGATTTTCACCTTTTCAAAATCTTTAGGTAGTAAAGTTAAATCTTA 60
QY 3272 TTTTAAAAAATAGATGAGTGTGGCTCATCGCTGTAATCCCAACACTTTGGGAAGCC 3331
Db 61 AAGGTCAAAGATTGCTGGGTATGGTAGCTCACGCCCTGTAAATTCCAACTCTTAGGAGGCC 120
QY 3332 GGGTCGGGAGGATAGCTTTGAGTCCAGCAGTGTGAGACCAAGTCAAGGCAACACAGCAAGAC 3391
Db 121 GAGCGGGCGTATCGCTTGAGCCAGGGGTTTGAGACCAAGTCAAGGCAACAGCAAGAC 180
QY 3392 CCATATCTAAAAAACAACAAACAAATTAATCTCTGGGTATGGTGTGCTCACCTGTA 3451

RESULT 11
US-10-301-480-1143654

US-10-301-480B-906314

Query Match 3.4%; Score 193.8; DB 19; Length 536;
Best Local Similarity 70.9%; Pred. No. 1.1e-16;
Matches 270; Conservative 1; Mismatches 108; Indels 2; Gaps 1;

QY 3212 ATCATGACATACGTTTAAATGATATATTTAAATAGCTTAGGCTATAAACCTTTTAAATTT 3271
DB 1 ATCTGTACAAAACATCTGATTTTCAAAATCTTTTAGGTAGTAAAGTTTAAATCTTA 60

QY 3272 TTTTAAAAAATAGATGAGTGTGGCTCATGCTGTAATCCCAACACTTTTGGGAAGCC 3331
DB 61 AAGGTCAAAGATTGCTGGGTATGAGTCAAGCTGTAATTTCCAACTCTAGGAGGCC 120

QY 3332 GGGTCGGGAGGATAGCTTGAAGTCCAGCAGTGTGAGACCAAGTCCAGGCAACACAGCAAGAC 3391
DB 121 GAGCGGGCGTATCGCTTGAGCCAGGGGTTTGAGACCAAGTAGGCAACAGGCAAAAC 180

QY 3392 CCCATATCTAAAAAACAACAAAAAATTAATCTGCTGGGTATGGTGTGCTCACTGTA 3451
DB 181 CCCATCTTACAAAATAAAAAATACA--ATAATGAGCTGGGCATGGTGGCAGCACCTGTG 238

QY 3452 GTCCAAAGCTACACGAAGCTCAGGCAGAAAGATCACTTTAGCCCGAGGAGTTGAGGCTG 3511
DB 239 GTCCAGCTACTTGGGAGGCTCAGGCAGGAGATGCTTTGAGCCAGGAGTTGGGGCTG 298

QY 3512 CAGTGATCCATGAACGCGCTGTACACTCAGTCTGGGTGACAGTGCAAGAAAGTGTCTCA 3571
DB 299 CAGTGAGCTGTGACTGTACTGTCACTCCACTAGGTGACAGATAAGACCTGTCTCA 358

QY 3572 AAAATAAATAAATAAAAA 3592
DB 359 AAAATAAATAAATAAAAA 379

RESULT 13

US-10-990-328A-94591/C
; Sequence 94591, Application US/10990328A
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001495
; CURRENT APPLICATION NUMBER: US/10/990,328A
; CURRENT FILING DATE: 2004-11-17
; NUMBER OF SEQ ID NOS: 558924
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94591
; LENGTH: 80503
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(80503)
; OTHER INFORMATION: n = A,T,C or G
US-10-990-328A-94591

Query Match 3.4%; Score 193.8; DB 15; Length 80503;
Best Local Similarity 66.5%; Pred. No. 5.5e-17;
Matches 276; Conservative 1; Mismatches 138; Indels 0; Gaps 0;

QY 3233 ATATTATTTAAATAGCTTAGGCTATAAACCTTTTAAATTTTAAAAAATAGATGAGTG 3292
DB 27708 AAAAAATTTAAATTTAGTAGAATAATATATTTTCAAAATGACAAAAGTTAGGCCACACA 27649

QY 3293 TGGTGGCTCATGCTGTAATCCCAACACTTTGGGAAGCCGGGTGCGGAGGATAGCTTGAG 3352
DB 27648 TGGTGGCTCACACCTGTAATCTCAGCACTTTTGAAGAGGCTGAGGCGGAGGAGCTGTTGAG 27589

QY 3353 TCCAGCAGTTTGAACCAAGTCCAGGCAACACAGCAAGACCCATATCTTAAAAAACAATA 3412
DB 27588 CCCAGGAGTTTGAACCAAGCTGGGCAACATAGCAAGACCCCTCTCTTATAAATAACAA 27529

QY 3413 CAAAAAATAATACCTGGGTATGTTGTCTCACTGTAGTCCAAGCTTACACAGGAAGCT 3472
DB 27528 GACAAATAATAGCAGGCGGTGGTGCATGCCTATGCTCCAGCTACTCAGGAGGCT 27469

QY 3473 GAGGCAAGAGATCACTTGAAGCCAGGAGGTTGAGGCTCAGTGATCCATGAACGCGCTG 3532
DB 27468 GAGGCAAGAGATCACTTGAAGCCAGGAGGTTGAGGCTCAGTGATCCATGAACGCGCTG 27409

QY 3533 CTACACTAGTCTGGGTGACAGTCAAGAGCTGTCTCAAAATATATAAATAAATAA 3592
DB 27408 TTGCACTGAGCTGGTGCAGAGCAAGACACTGTCTCCAAAAAATAAATAAATAA 27349

QY 3593 TAACTTTTAAAAAACAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3647
DB 27348 AAGGTTAAACCGCACATGCATAATTTGTTAGAGCAAAATATCATCTGAAAAAT 27294

RESULT 14

US-09-925-065A-552294
; Sequence 552294, Application US/09925065A
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 552294
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-552294

Query Match 3.4%; Score 192.2; DB 7; Length 536;
Best Local Similarity 70.6%; Pred. No. 1.8e-16;
Matches 269; Conservative 1; Mismatches 109; Indels 2; Gaps 1;

QY 3212 ATCATGACATACGTTTAAATGATATTTAAATACGTTAGGCTATAAACCTTTTAAATTT 3271
DB 1 ATCTGTACAAAACATCTGATTTTCAAAATCTTTAGGTAGTAAAGTTTAAATCTTA 60

QY 3272 TTTTAAAAAATAGATGAGTGTGGTCTCATGCTGTAATCCCAACACTTTTGGGAAGCC 3331
DB 61 AAGGTCAAAGATTGCTGGGTATGCTGCTCAGCCTGTAATTTCAACACTCTAGGAGGCC 120

QY 3332 GGGTCGGGAGGATAGCTTTGAGTCCAGCAGTGTGAGACAGTCCAGGCAACACAGCAAGAC 3391
DB 121 GAGCGGGCGTATCGCTTGAGCCAGGGGTTTGAGACAGTCCAGGCAACAGGCAAAAC 180

QY 3392 CCCATATCTAAAAAACAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3451
DB 181 CCCATCTTACAAAATAAAAAATACA--ATAATGAGCTGGGCATGGTGGCAGCACCTGTG 238

QY 3452 GTCCAAAGCTACACAGGAGTGTGAGGCAAGAGGATCACTTTGAGCCAGGAGGTTGAGGCTG 3511
DB 239 GTCCAGCTACTTGGGAGGCTGAGGCAAGGAGTGGCTTGAGCCAGGATGTTGGGGCTG 298

QY 3512 CAGTGATCCATGAACGCGCTGTCTACACTCAGTCTGGGTGACAGTGCAAGAAAGTGTCTCA 3571
DB 299 CAGTGAGCTGTGACTGTACTGTCACTCCACTAGGTGACAGATAAGACCCCTGTCTCA 358

3572 AAAATAATAATAATAATAAAA 35922
QY
159 AAAATAAACAAATTAATAATAA 379
DB

RESULT 15

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RES001.15
US-10-301-480C-906313
; Sequence 906313, Application US/10301480C
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of
; Nucleotide Polymorphisms
; FILE REFERENCE: 108827-137
; CURRENT APPLICATION NUMBER: US/10/301.480C
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ IDS: 989478
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 906313
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480C-906313

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Query Match	3.4%	Score	192.2	DB	10	Length	536
Best Local Similarity	70.6%	Ident. No.	1.8e-16				
Matches	269	Conservative	1	Mismatches	109	Indels	2
Gaps	1						
QY	3212	ATCATGACATACGTTTAAATGATATATTAAATACGTTAGGCTATAAACCTTTTAAATT	3271	DB	1	ATCTGTACAAACATCTGNTTTCACCTTTTCAAAATCTTTAGGTAGTAAAGTTAAATCTA	60
QY	3272	TTTTAAAAAATAGATGAGTGTGGTGCATGCTGTAAATCCCAACACTTTTGGGAAGCC	3331	QY	3332	GGTCCGGAGGATAGCTTCAGTCCAGCAGTTTTGAGACAGTCAAGGCAACACAGCAAGAC	3391
DB	61	AAGGTCAAAGATTGCTGGGTATGGTAGTTCACGCTGTAAATCCCAACACTCTAGAGGCC	120	DB	121	GAGCGGGGCTATCGCTTGAGCCAGGGGTTTGAGACCAGCTAGGCAACAAAGGCAGAAAC	180
QY	3392	CCCATATCTAAAAAACAACAAAAATTA	3451	QY	3452	GTCCACGCTACACAGGAGCTGAGGCAGAAAGATACATTTGAGCCAGGAGGTGAGGCTG	3511
DB	181	CCCATCTCTACAAATAAAAAATACA--ATAATGAGCTGGGCATGTGGCAGCCACTGTG	238	DB	239	GTCCCAGCTACTTTGGGAGGCTGAGGCAGGAGGATGCGCTTTGAGCCAGGATGTGGGGCTG	298
QY	3512	CAGTGATCCATGAACGGCTGTCTACACTCACTGTGGGTGACAGTGCAGAACTGTCTCA	3571	QY	299	CAGTGAGCTGTGACTGTACTTGCATCCACCTAGGTGACAGAAATAGACCCCTGTCTCA	358
DB	3572	AAAATAATAATAATAAAAA	3592	QY	359	AAAAAACAACATAAAAAATAA	379

Search completed: November 2, 2005, 03:44:26
Job time : 7601 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 1, 2005, 14:41:22 ; Search time 847 Seconds
(without alignments)
10965.179 Million cell updates/sec

Title: US-10-030-294-1
Perfect score: 5676
Sequence: 1 cagctgttcaggatgtctg.....tttataattgttctccgt 5676

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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- 2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1987.4	35.0	255679	4	US-09-949-016-17189
2	190.6	3.4	265038	4	US-09-949-016-15779
3	187.6	3.3	8133	3	US-09-659-791A-10
c 4	186.4	3.3	601	4	US-09-949-016-142852
5	186	3.3	17348	4	US-09-949-016-17403
c 6	185.6	3.3	601	4	US-09-949-016-201827
c 7	185.4	3.3	37292	4	US-09-949-016-15382
8	184.8	3.3	172677	4	US-09-949-016-13444
9	184.6	3.3	33272	4	US-09-949-016-16949
10	184.4	3.2	601	4	US-09-949-016-58699
11	184	3.2	601	4	US-09-949-016-132156
12	183.4	3.2	601	4	US-09-949-016-119415
c 13	182.8	3.2	36228	4	US-09-949-016-12256
c 14	182.6	3.2	36228	4	US-09-949-016-15458
c 15	182.6	3.2	134140	4	US-09-949-016-12672
c 16	182.6	3.2	134241	4	US-09-949-016-12424
c 17	182.6	3.2	134242	4	US-09-949-016-15813
c 18	182.6	3.2	134242	4	US-09-949-016-15814
c 19	182.6	3.2	134242	4	US-09-949-016-15815
c 20	182.4	3.2	601	4	US-09-949-016-132157
21	182.2	3.2	36651	3	US-09-738-894A-3
22	182.2	3.2	36651	4	US-09-964-469-3
23	182.2	3.2	51403	4	US-09-949-016-115057
c 24	181.8	3.2	4732	4	US-09-949-016-14962
25	181	3.2	601	4	US-09-949-016-127367
26	181	3.2	69924	4	US-09-949-016-15367
27	180.8	3.2	21920	4	US-09-949-016-15609

c	28	180.2	3.2	86273	4	US-09-949-016-15273	Sequence 15273, A
	29	180.2	3.2	87205	4	US-09-949-016-13430	Sequence 13430, A
	30	180	3.2	78720	4	US-09-949-016-12710	Sequence 12710, A
	31	180	3.2	78720	4	US-09-949-016-17283	Sequence 17283, A
	32	179.6	3.2	103377	4	US-09-949-016-14089	Sequence 14089, A
	33	179.6	3.2	119032	4	US-09-949-016-12160	Sequence 12160, A
	34	179.6	3.2	119032	4	US-09-949-016-17268	Sequence 17268, A
	35	179.6	3.2	163181	4	US-09-949-016-13730	Sequence 13730, A
	36	179.4	3.2	601	4	US-09-949-016-58698	Sequence 58698, A
c	37	179.2	3.2	77851	4	US-09-949-016-12508	Sequence 12508, A
c	38	179.2	3.2	77867	4	US-09-949-016-13211	Sequence 13211, A
c	39	179.2	3.2	77867	4	US-09-949-016-13212	Sequence 13212, A
c	40	179.2	3.2	77940	4	US-09-949-016-12509	Sequence 12509, A
	41	179	3.2	65848	4	US-09-949-016-13285	Sequence 13285, A
c	42	178.8	3.2	152132	4	US-09-949-016-13845	Sequence 13845, A
c	43	178.8	3.2	152145	4	US-09-949-016-12371	Sequence 12371, A
c	44	178.6	3.1	186734	4	US-09-949-016-14870	Sequence 14870, A
c	45	178.6	3.1	193689	4	US-09-949-016-12350	Sequence 12350, A

ALIGNMENTS

RESULT 1

US-09-949-016-17189
; Sequence 17189, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17189
; LENGTH: 255679
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(255679)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17189

Query Match		35.0%	Score 1987.4;	DB 4;	Length 255679;
Best Local Similarity		99.9%	Pred. No. 0;		
Matches 1999;		Conservative	0;	Mismatches	1;
				Indels	1;
				Gaps	1;
Qy	3676	TATCCCTGGAAGTAAATTTTAAAGAGAGTTCCTTCCTCATTTCTAGAGAGCTC	3735		
Db	1	TATCCCTGGAAGTAAATTTTAAAGAGTTCCTTCCTCATTTCTAGAGAGCTC	60		
Qy	3736	GAATTGTAAATATACAGAGCTAGAGAACTAGGCGTCCCACTCCAAAGTGTGTCCA	3795		
Db	61	GAATTGTAAATATACAGAGCTAGAGAACTAGGCGTCCCACTCCAAAGTGTGTCCA	120		
Qy	3796	AGGACAGAGAGCATCAAGTAACCTGGGAGCTGTAGAATGCAGAGTCTTAGGCGCTCAC	3855		
Db	121	AGGACAGAGAGCATCAAGTAACCTGGGAGCTGTAGAATGCAGAGTCTTAGGCGCTCAC	180		
Qy	3856	CCGAGACCTACTGAACACAGAAATCTGCATTAAACAGATTTTCTAGGTGCCTCAGCGGCACAT	3915		
Db	181	CCGAGACCTACTGAACACAGAAATCTGCATTAAACAGATTTTCTAGGTGCCTCAGCGGCACAT	240		
Qy	3916	TAAACTTGGAAGCTCTGCACATAGAAATCTTCACTCCACCTTTTCATTATAAATGGAAATC	3975		

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Db 241 TAAACTTGAGAGCTCTGACCTAGAAATCTTCACTCCACCTTTCATTATAAATGGAATC 300
QY 3976 ACTTGGGCTGTGTGCAGAGAAATATGATATATTTTAAATTTTCAGAACTTCTATTTAGGTC 4035
Db 301 ACTT-GGCTGTGTGCAGAGAAATATGATATATTTTAAATTTTCAGAACTTCTATTTAGGTC 359
QY 4036 ATCTATATTTGCTAAATAGCAGGGAAGAAAGCCAAACTCTTTAACTGCAATTAACAAATCT 4095
Db 360 ATCTATATTTGCTAAATAGCAGGGAAGAAAGCCAAACTCTTTAACTGCAATTAACAAATCT 419
QY 4096 ATAATTAATTAAGTAAAGCAATCTTCCCTTTAAGTTTTCATATTTTGGAGCAAGCTGTTT 4155
Db 420 ATAATTAATTAAGTAAAGCAATCTTCCCTTTAAGTTTTCATATTTTGGAGCAAGCTGTTT 479
QY 4156 GATTTGGCTGGGCTCAGGCGGCTGTGTTGTGAATTTCAATTTACAGATGTTAGCCG 4215
Db 480 GATTTGGCTGGGCTCAGGCGGCTGTGTTGTGAATTTCAATTTACAGATGTTAGCCG 539
QY 4216 CTCTCGGCTTAAGTAAAGGAAGAAATGTCGAAGTTTAAATAGCTTCTCCCTTCCATCCT 4275
Db 540 CTCTCGGCTTAAGTAAAGGAAGAAATGTCGAAGTTTAAATAGCTTCTCCCTTCCATCCT 599
QY 4276 GGCTGAAGCAACAAATAAATAATTTTATGAACACATTTTGAATTTAGTATTACTTACAG 4335
Db 600 GGCTGAAGCAACAAATAAATAATTTTATGAACACATTTTGAATTTAGTATTACTTACAG 659
QY 4336 GGAATGTCAAAATCTCTGAAAGGGCTTTAGATTTGTCACAACTTTGACATCTACTGA 4395
Db 660 GGAATGTCAAAATCTCTGAAAGGGCTTTAGATTTGTCACAACTTTGACATCTACTGA 719
QY 4396 TGTCACTATTTACAGGTGTCTGTGACTAGGGGTGAAGGAAGATGTGAACCTCACC 4455
Db 720 TGTCACTATTTACAGGTGTCTGTGACTAGGGGTGAAGGAAGATGTGAACCTCACC 779
QY 4456 ATGTTAGTGAACGTTAGATACAGAGTGGTTTTTTTCCCTGTTGGAGTCTATCCTA 4515
Db 780 ATGTTAGTGAACGTTAGATACAGAGTGGTTTTTTTCCCTGTTGGAGTCTATCCTA 839
QY 4516 ACTGAGCTTCTGAATCTATTTCAATTTCAATTTCAAAATCCAAATCCAGGATTAAGTTTA 4575
Db 840 ACTGAGCTTCTGAATCTATTTCAATTTCAATTTCAAAATCCAAATCCAGGATTAAGTTTA 899
QY 4576 CAGCCCATATTCAGAAAGGAAATAAATAATTTTGTGTGTAGACTTTCTCTATATTAACAT 4635
Db 900 CAGCCCATATTCAGAAAGGAAATAAATAATTTTGTGTGTAGACTTTCTCTATATTAACAT 959
QY 4636 GATTTGGGAATATATGAACAAATTTTATGGTTTCTTTTCGAAGTAGGTCAAGTCAAAGCAA 4695
Db 960 GATTTGGGAATATATGAACAAATTTTATGGTTTCTTTTCGAAGTAGGTCAAGTCAAAGCAA 1019
QY 4696 AACCAAAACAGCAAAACCTGTAAGACATAAAGATAGAGTGAGCGGACTGAGATTA 4755
Db 1020 AACCAAAACAGCAAAACCTGTAAGACATAAAGATAGAGTGAGCGGACTGAGATTA 1079
QY 4756 AAATAAATAGATATATTTTATTAACAGGCAATTTGAAATAATTTGTGCATTTCAAGATA 4815
Db 1080 AAATAAATAGATATATTTTATTAACAGGCAATTTGAAATAATTTGTGCATTTCAAGATA 1139
QY 4816 TTCTACAATAATATATTTTCCAAATTTTAAATATCTTTTAAAGAAATTTACTATATPATG 4875
Db 1140 TTCTACAATAATATATTTTCCAAATTTTAAATATCTTTTAAAGAAATTTACTATATPATG 1199
QY 4876 TAAGTACATGTGCATGTTTGGAGTAGGATATTTAACTCAATAAAGGTTATTTTCTTTT 4935
Db 1200 TAAGTACATGTGCATGTTTGGAGTAGGATATTTAACTCAATAAAGGTTATTTTCTTTT 1259
QY 4936 ATTCGGGTCAAGCAAGCTTCTAAGGGGATGTGAAGGGATATCTCTTTCTTTAGCTGA 4995
Db 1260 ATTCGGGTCAAGCAAGCTTCTAAGGGGATGTGAAGGGATATCTCTTTCTTTAGCTGA 1319
QY 4996 GAGGAAGAGTGAGTCTTAAGTTTAAATATAATCAAGGAATTTCCCTGCTTTGCTATTGA 5055
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Db 1320 GAGGAAGAGTGAGTCTTAAGTTTAAATATAATCAAGGAATTTCCCTGCTTTTGTCTATTGA 1379
QY 5056 GATTGTGACCAACAAGGCGGTTGGCTGAAAGGGAACCTGAAGGGCGGGAGGGAGGAA 5115
Db 1380 GATTGTGACCAACAAGGCGGTTGGCTGAAAGGGAACCTGAAGGGCGGGAGGGAGGAA 1439
QY 5116 ATAGATGAAAAACAAAAACAAAACTTCCCTAAGCAGCTCTACAAAAACATTTTAGC 5175
Db 1440 ATAGATGAAAAACAAAAACAAAACTTCCCTAAGCAGCTCTACAAAAACATTTTAGC 1499
QY 5176 CCAGAAATAGTCACAGAAATCTTCAAAATCAAAACCAAGTATCCAGATACAAAGGAAGTTTA 5235
Db 1500 CCAGAAATAGTCACAGAAATCTTCAAAATCAAAACCAAGTATCCAGATACAAAGGAAGTTTA 1559
QY 5236 TGTAGCTGAGCAGGGGTGACACTCATCAGCTCAGTTCAGTTTCAAAAGTCCAGGCTGCT 5295
Db 1560 TGTAGCTGAGCAGGGGTGACACTCATCAGCTCAGTTCAGTTTCAAAAGTCCAGGCTGCT 1619
QY 5296 GAAATTTAAACTCTGATGCCAATTCATGCCAGCATCCAATCACGACAGAGATCAGAAGTTCA 5355
Db 1620 GAAATTTAAACTCTGATGCCAATTCATGCCAGCATCCAATCACGACAGAGATCAGAAGTTCA 1679
QY 5356 GAGATCCCTCCAGCTCCAAATTCGCAACAAAGTGTGGCTACTATACGTCAGGACTCT 5415
Db 1680 GAGATCCCTCCAGCTCCAAATTCGCAACAAAGTGTGGCTACTATACGTCAGGACTCT 1739
QY 5416 GAAGCCGTGAGAGGGGGAAGAACAAAGTAGAGAGGATGCCAGCTGTAAGATCGA 5475
Db 1740 GAAGCCGTGAGAGGGGGAAGAACAAAGTAGAGAGGATGCCAGCTGTAAGATCGA 1799
QY 5476 GTGTTTATGAAGTTTGTAGTCAATTTGATGAATCTCATTTGGCTAAATCAAGAAACCGTCCG 5535
Db 1800 GTGTTTATGAAGTTTGTAGTCAATTTGATGAATCTCATTTGGCTAAATCAAGAAACCGTCCG 1859
QY 5536 CTTCTTTGCAAAATATGATGAAGGAGAGAGTGCCTAAATCTCTATGCTGATAGCATTT 5595
Db 1860 CTTCTTTGCAAAATATGATGAAGGAGAGAGTGCCTAAATCTCTATGCTGATAGCATTT 1919
QY 5596 GACCTTATGCTTTTAGCTCCCGCTTTATATCTATATATACACAGGATTTTGTGTATA 5655
Db 1920 GACCTTATGCTTTTAGCTCCCGCTTTATATCTATATATACACAGGATATATGTGTATA 1979
QY 5656 TTTTATATAATTTGTTCTCCGT 5676
Db 1980 TTTTATATAATTTGTTCTCCGT 2000

RESULT 2
US-09-949-016-15779
; Sequence 15779, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FabSeq for Windows Version 4.0
; SEQ ID NO 15779
; LENGTH: 265038
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(265038)
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1 GENERAL INFORMATION: J. Craig et al.
 2 APPLICANT: VENTER, J. Craig et al.
 3 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 4 WITH HUMAN DISEASES, METHODS OF DETECTION AND USES THEREOF
 5 TITLE OF INVENTION: WITH HUMAN DISEASES, METHODS OF DETECTION AND USES THEREOF
 6 FILE REFERENCE: CL001307
 7 CURRENT APPLICATION NUMBER: US/09/949,016
 8 CURRENT FILING DATE: 2000-04-14
 9 PRIOR APPLICATION NUMBER: 60/241,755
 10 PRIOR FILING DATE: 2000-10-20

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; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17403
; LENGTH: 17348
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17403

Query Match          3.3%; Score 186; DB 4; Length 17348;
Best Local Similarity 74.3%; Pred. No. 11e-32;
Matches 248; Conservative 0; Mismatches 85; Indels 1; Gaps 1;

QY 3264 TTTAAATTTTAAAAAATAGATGAGTGGTGGCTCATGCTGTAATCCCAACACTTT 3323
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
8546 TTTAAAGAGGAAAAAACTGAGCTGGGCATGGTGGCTCATGCTGTGATGCCAGCACTTT 8605
QY 3324 GGAAGCGGGTCGGGAGGATAGCTTGAATCCAGCACTTTGAGACAGTCAGGCAACAC 3383
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
8606 GAGAGCCCAAGCGGGAGGATCATTTTGAAGCCAGGAGTTTGAAGACCAAGCTGGCCAAGAT 8665
QY 3384 AGCAAGACCCCATATCTTAAAAAACAACAAAAACAACAAAAATTAACCTGGGTATGTTGCT 3443
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
8666 AGTGAGACCCCTGCTCTACAAAATAAAAAATTTAAAAAATTAGCCGGTGTGGTGTGCA 8725
QY 3444 CACCTGTAGTCCAAGCTACACAGAAAGCTGAGGCAAGGATCACTTTGAGCCCAAGGAT 3503
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
8726 CACCTGTAGTCTCAGCTACTCGGGAGGCTGAGGCAAGAGTCACTTGAGCCCTGGAAGTT 8785
QY 3504 TGAGGCTGCAGTATCATGAACGCGCTGTACACT-CAGTCTGGGTGACAGTCAAGAA 3562
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
8786 GGAGGCTGCAGTATGATGTCACCTATGTCATTCAGCCCTGGGCAACAGAGTGAGAC 8845
QY 3563 GCTGTCTCAAAAATAATAATAATAATAATAATAAC 3596
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
8846 CTTGCTGTAAATTTAAAAAATAATAATAATAATAAC 8879

RESULT 6
US-09-949-016-201827/c
; Sequence 201827, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201827
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-201827

Query Match          3.3%; Score 185.6; DB 4; Length 601;
Best Local Similarity 74.0%; Pred. No. 3.2e-33;
Matches 247; Conservative 1; Mismatches 85; Indels 1; Gaps 1;

QY 3264 TTTAAATTTTAAAAAATAGATGAGTGGTGGCTCATGCTGTAATCCCAACACTTT 3323
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
466 TTTAAAGAGGAAAAAACTGAGCTGGGCATGGTGGCTCATGCTGTGATGCCAGCACTTT 407
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QY 3324 GGAAGCCGGTCGGGAGGATAGCTTTGAGTCCAGCAGTTTGAACCAAGTCAGGCAACAC 3383
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
406 GAGAGCCCAAGCGGGAGGATCATTTTGAAGCCAGGAGTTTGAACCAAGTCAGGCAACAT 347
QY 3384 AGCAAGACCCCATATCTTAAAAAACAACAAAAACAACAAAAATTAACCTGGGTATGTTGCT 3443
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
346 AGTGAGACCCCTGCTCTACAAAATAAAAAATTTAAAAAATTAGCCRGGTGTGGTGTGCA 287
QY 3444 CACCTGTAGTCCAAGCTACACAGAAAGCTGAGGCAAGGATCACTTTGAGCCCAAGGAT 3503
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
286 CACCTGTAGTCTCAGCTACTCGGGAGGCTGAGGCAAGAGTCACTTGAGCCCTGGAAGTT 227
QY 3504 TGAGGCTGCAGTATCATGAACGCGCTGTACACT-CAGTCTGGGTGACAGTCAAGAA 3562
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
226 GGAGGCTGCAGTATGATGTCACCTATGTCATTCAGCCCTGGGCAACAGAGTGAGAC 167
QY 3563 GCTGTCTCAAAAATAATAATAATAATAATAATAAC 3596
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
166 CTTGCTGTAAATTTAAAAAATAATAATAATAATAAC 133

RESULT 7
US-09-949-016-15382/c
; Sequence 15382, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15382
; LENGTH: 37292
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(37292)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15382

Query Match          3.3%; Score 185.4; DB 4; Length 37292;
Best Local Similarity 74.9%; Pred. No. 2e-32;
Matches 245; Conservative 0; Mismatches 81; Indels 1; Gaps 1;

QY 3284 AGATGAGTGTGGTGCATGCTGTAATCCCAACACTTTGGGAAGCCGGGTGGGAGGA 3343
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
15021 AGTTGAGTGTGGTGCCTCAGCCTGAAATCCCAAGCACTTTGGGAGGCCAAGGTGGAGAA 14962
QY 3344 TAGCTTGAAGTCCAGCAGTTTGAAGCAGTCAAGGCAACACAGCAAGCCCATATCTAAA 3403
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
14961 TTGCCTGAGGCCAGGAGTTCAAGAGCCAGCCTGGGCAACATAGCAAGACCTATCTCTACA 14902
QY 3404 AAAACAAAAACAACAAAAATTAACCTGGGTATGTTGCTCACCTGTAGTCCAAGCTACA 3463
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
14901 AAAATTTAAAAATAAAAAAGTAGCTGAGTGTGGTGACGTGCTCTGTTGCCAACCACT 14842
QY 3464 CAGGAAGCTGAGGCAAGGATCACTTTGAGCCCAAGGAGTTGAGGCTGAGTCGATCCATG 3523
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
14841 CAGGAGCTGAGGTGGGAGGATTTGCTTGAGCCCAAGGAGTTTGAAGCTGAGTGATG 14782
QY 3524 AACGCGCTCTACACT-CAGTCTGGGTGACAGTCAAGAGCTGTCTCAAAAATAATAAA 3582
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 14781 ATCACGACACTGGCTCCAGCTTGGTGACAGTGAGACCTTGCTCTAAAAAAAAAAAG 14722
QY 3583 TAAATATAAATAAATCTTTTAAAAACAA 3609
Db 14721 AAAAGAAAAAAGAAAAAGAAATGATAA 14695

RESULT 8
US-09-949-016-13444
; Sequence 13444, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13444
; LENGTH: 172677
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13444

Query Match 3.3%; Score 184.8; DB 4; Length 172677;
Best Local Similarity 69.6%; Pred. No. 5.3e-32;
Matches 281; Conservative 0; Mismatches 117; Indels 6; Gaps 2;

QY 3195 AAATAACAACACTTGAATCATGACATACGTTAAATCATATATTAAATACGTGAGC 3254
Db 92789 AATTTAAAAATATTACAAAATCATACAAATAGATGTTGAGTTAAATCAATTCAGTTGAC 92848
QY 3255 TATAAACCTTTTAAATTTTTTAAAAAATAGAT-----GAGTGTGGTGGCTCATGCCCTGT 3309
Db 92849 TTTTGTGATTTGGTATTTTAAAAAAGAAATGACCATGTGTGGTGGCTCGTGTCTGT 92908
QY 3310 AATCCCAACACTTTGGGAAGCGGGTCGGAGGATAGCTTGAGTCCAGCAGTTTGAGACC 3369
Db 92909 AATCCAGCACTTTGGAAGCTGAGTTGGAAGGATAGCTTGAGACCAGGAGTTTGAGACC 92968
QY 3370 AGTCAGGCAACACAGCAAGACCCCATATCTAAAAAACAACAAACAAATTTACCTG 3429
Db 92969 AGCCTGGCAACATGGCAAGACCTCATCTACTAAAAAATAAAAAATAAAGCTA 93028
QY 3430 GGTATGTTGTGCTCACCTGTAGTCCAGTACACAGGAAGCTGAGGACAGGAGGATCACT 3489
Db 93029 GGCATAGCAGTGTGTTCATATAGTCCCAGCTACTCAGAGGACACAGGTGGGAGGATCGCT 93088
QY 3490 TGAGCCAGGAGGTGAGGCTGCGAGTGATCCATGAACGCGCTGCTPACACT-CAGTCTGGG 3548
Db 93089 TGAACCCAGGAGGTGAGGCTGCGAGTGAGCTGTGATCACACCACTGCACTCCAGCCTAGG 93148
QY 3549 TGACAGTCACAGAGCTGTCTCAAAATAATAATAATAAAAA 3592
Db 93149 TGACAGAGAAAGACCTTGCTCTCAAGAATAAGCAACAAAAATAA 93192

RESULT 9
US-09-949-016-16949
; Sequence 16949, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16949
; LENGTH: 33272
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16949

Query Match 3.3%; Score 184.6; DB 4; Length 33272;
Best Local Similarity 68.6%; Pred. No. 2.9e-32;
Matches 300; Conservative 0; Mismatches 129; Indels 8; Gaps 3;

QY 3170 TTAGCTTAGTAACCTTTAGGATTTTTTAAATAACAACACTATTGAAATCATGACATACGTTTAA 3229
Db 31344 TTGCTTATAAGTTTTTCTCAATATTGTGAATAAACTTCCACATCGTAGATACATGTCC 31403
QY 3230 ATGATATTATTAAATACGTTTAGGCTATATAAACCTTTTAAATTTTTTAAAAAATAGATGA 3289
Db 31404 ATAAATTTTTTTTGTATTGTTTTTGAATTTTA--TTAAATTTTATTGAAATATAGCTGG 31460
QY 3290 GTGTGGTGGCTCATGCCCTGTAATCCAAACACTTTTGGGAAGCGGGTCGGAGGATAGCTT 3349
Db 31461 GTGCAGTGGCTTACCTCTGTAAATCCCAACACTTTTGAGAGGCTGAGGTGGGATGATTCCTT 31520
QY 3350 GAGTCCACAGCTTTGAGACCACTGAGGCAACACAGCAAGACCCCATATCTAAAAAACA 3409
Db 31521 GAGTCCAGGAGTTCAAGACCACTTGGGCAACACAGCAGATACATCTCTTACAAAAA 31580
QY 3410 AAACAAAAAATAATTTACCTGGGTATGTTGTCTCACCTGTAGTCCAAAGCTACACAGGAA 3469
Db 31581 ATAGA---AAAATTAGCTGGCATGGTGGCTGTGCTGTAGTCCAGCTACTCGGAG 31636
QY 3470 GCTGAGCAGAGGATCACTTTGAGCCAGGAGGTGAGGCTGCAGTGATCCATGACCGG 3529
Db 31637 GCTGAGCGGGGGATCACTTTGAGCCAGGAGGTGAGGCTGCAGTGATCTAGGATTGCA 31696
QY 3530 CTGCTACACT-CAGTCTGGGTGACAGTGCAAGAGAGCTGTCTCAAAAAATAATAATAAATA 3588
Db 31697 CTGCTGCACTCCAGCGTGGGTGACAGCAGACCCCTGTCTCAAAAAACCCCAAAAAACA 31756
QY 3589 AAAATAAATTTTAAAAA 3605
Db 31757 AACTGAAATATCAANA 31773

RESULT 10
US-09-949-016-58699
; Sequence 58699, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16949
; LENGTH: 33272
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-58699
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; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16949
; LENGTH: 33272
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16949

Query Match 3.3%; Score 184.6; DB 4; Length 33272;
Best Local Similarity 68.6%; Pred. No. 2.9e-32;
Matches 300; Conservative 0; Mismatches 129; Indels 8; Gaps 3;

QY 3170 TTAGCTTAGTAACCTTTAGGATTTTTTAAATAACAACACTATTGAAATCATGACATACGTTTAA 3229
Db 31344 TTGCTTATAAGTTTTTCTCAATATTGTGAATAAACTTCCACATCGTAGATACATGTCC 31403
QY 3230 ATGATATTATTAAATACGTTTAGGCTATATAAACCTTTTAAATTTTTTAAAAAATAGATGA 3289
Db 31404 ATAAATTTTTTTTGTATTGTTTTTGAATTTTA--TTAAATTTTATTGAAATATAGCTGG 31460
QY 3290 GTGTGGTGGCTCATGCCCTGTAATCCAAACACTTTTGGGAAGCGGGTCGGAGGATAGCTT 3349
Db 31461 GTGCAGTGGCTTACCTCTGTAAATCCCAACACTTTTGAGAGGCTGAGGTGGGATGATTCCTT 31520
QY 3350 GAGTCCACAGCTTTGAGACCACTGAGGCAACACAGCAAGACCCCATATCTAAAAAACA 3409
Db 31521 GAGTCCAGGAGTTCAAGACCACTTGGGCAACACAGCAGATACATCTCTTACAAAAA 31580
QY 3410 AAACAAAAAATAATTTACCTGGGTATGTTGTCTCACCTGTAGTCCAAAGCTACACAGGAA 3469
Db 31581 ATAGA---AAAATTAGCTGGCATGGTGGCTGTGCTGTAGTCCAGCTACTCGGAG 31636
QY 3470 GCTGAGCAGAGGATCACTTTGAGCCAGGAGGTGAGGCTGCAGTGATCCATGACCGG 3529
Db 31637 GCTGAGCGGGGGATCACTTTGAGCCAGGAGGTGAGGCTGCAGTGATCTAGGATTGCA 31696
QY 3530 CTGCTACACT-CAGTCTGGGTGACAGTGCAAGAGAGCTGTCTCAAAAAATAATAATAAATA 3588
Db 31697 CTGCTGCACTCCAGCGTGGGTGACAGCAGACCCCTGTCTCAAAAAACCCCAAAAAACA 31756
QY 3589 AAAATAAATTTTAAAAA 3605
Db 31757 AACTGAAATATCAANA 31773

RESULT 10
US-09-949-016-58699
; Sequence 58699, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16949
; LENGTH: 33272
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16949
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; SEQ ID NO 58699
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-58699

Query Match      3.2%; Score 184.4; DB 4; Length 601;
Best Local Similarity 69.3%; Pred. No. 6.1e-33;
Matches 280; Conservative 1; Mismatches 117; Indels 6; Gaps 2;

QY 3195 AAATAACAACCTATTGAATCATGACATACGTTTAAATGATATTTAAATACGTTAGGC 3254
Db 156 AATTAAATAATATTACAAATCATACACATAGATGTTGAGTTAAATTCATTTCAATTTGAC 215
QY 3255 TATAAACCCTTTTAAATTTTTTAAAAAATAGAT-----GAGTGTGGTGGCTCATGCCCTGT 3309
Db 216 TTTTGTGATTTGGTATTTTTTTTAAAAAAGATTTGACCATGTGTGGTTCGTCGTGT 275
QY 3310 AATCCCAACACTTTGGGAAGCGGGTCGGGAGGATAGCTTGAGTCCAGCAGTTTGAGACC 3369
Db 276 AATCCAGCACTTTGGAAAGCTGAGYTGGAAGGATAGCTTGAGACCAGGAGTTTGAGACC 335
QY 3370 AGTCAGGCAACACAGCAAGACCCCATATCTTAAAAAACAACAAACAAATTTACCTG 3429
Db 336 AGCTGTGGCAACATGGCAAGACCTCATCTCTACTAAAAATAAAAATAAAAAATAAGCTA 395
QY 3430 GGTATGGTTGTGCTCACCTGTAGTCCAAAGCTACACAGGAAGCTGAGGAGGAGGATCACT 3489
Db 396 GGCATAGCAGTGTGTTTCATATAGTCCAGCTACTCAGGAGGCACAGGTGGGAGGATCGCT 455
QY 3490 TGAGCCCAAGAGGTTGAGGCTGACGTATCCATGAACCGGCTGTACACT-CAGTCTGGG 3548
Db 456 TGAACCCAGGAGTTGAGGCTGAGCTGAGCTGATCAACACACTGCACCTCCAGCCTAGG 515
QY 3549 TGACAGTCAAGAACTGTCTCAAAATAATAATAATAATAAAA 3592
Db 516 TGACAGAGAAAGACCTTGTCTCAAGAAATAAGCAACAAATAAA 559

RESULT 11
US-09-949-016-132156
; Sequence 132156, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 132156
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-132156

Query Match      3.2%; Score 184; DB 4; Length 601;
Best Local Similarity 62.4%; Pred. No. 7.5e-33;
Matches 322; Conservative 1; Mismatches 186; Indels 7; Gaps 2;

QY 3195 AAATAACAACCTATTGAATCATGACATACGTTTAAATGATATTTAAATACGTTAGGC 3254
Db 5 ACACACACACACACACAAAGATAAAGTGGACTTTTAAAGCTTAAAGCTTAAAGCTTCAA 64
QY 3255 TATAAACCCTTTTAAATTTTTTAAAAAATAAGATGAGTGTGGCTCATGCTGTATATCC 3314
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Db 65 AAGATACCAATAAGAAAAATGAAAAAGGCAGGTCAGGTGGCTCAGCCCTGTATATCC 124
QY 3315 CAACACTTTGGGAAGCGGGTCGGGAGGATAGCTTTCAGTCCAGCAGTTTTCAGACCCAGTCA 3374
Db 125 CACCACCTTTGGGAGGCGGAGGCGGGGATTTGCTTTGAGGCCAGAGTTTCAGACCCAGTCT 184
QY 3375 GGCAACACACAGCAAGACCCCATATCTAAAAAACAACAAAAACAAATTTACCTGGGTAT 3434
Db 185 GGCCAAACATGGCAAAACCCCTCTCT-----ACTAAAAATACAAAAATTTAGCCTGGTGT 238
QY 3435 GGTGTGCTCACCTGTAGTCCAAAGCTACACAGGAAGCTGAGGAGGAGGATCACTTCAGC 3494
Db 239 GTTGGCGGCACCTGTAAATCCAGTTACTCAGGAGGCTGAGGAGGAGGAGGATTCGCTTGAAC 298
QY 3495 CCAGGAGGTTGAGGCTCAGTGCATGAACCGGCTGTACACT-CAGTCTCGGTGACA 3553
Db 299 CCRGAGGCGAGAGGTTGCGAGTGAGCCAGATCAGCCGTTGCACCTCAGCCAGGCGGACA 358
QY 3554 GTGCAAGCAAGCTGTCTCAAAAAATAATAATAATAATAATAATAATAATAATAATAATA 3613
Db 359 GAGCAAACTCCATCTCAAAAAAATAATAATAATAATAATAATAATAATAATAATAATAA 418
QY 3614 TAATTAATTTTAAAAACACACACTAGAGATGTTTGCNAATGATTTTGGGAGTC 3673
Db 419 TCAATGAATAGATAAAATATTTGCAAAATCATATATCTGATAAGGACCTGTATCTAGAA 478
QY 3674 TATATCCCTGGAAGTTAATTTAAATATTTTAGAAGA 3709
Db 479 TATAAAAAAGAAATTTCTGTAACTCAATTAATAAGAAGA 514
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RESULT 12
US-09-949-016-119415
; Sequence 119415, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119415
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-119415

Query Match      3.2%; Score 183.4; DB 4; Length 601;
Best Local Similarity 62.2%; Pred. No. 1e-32;
Matches 304; Conservative 1; Mismatches 182; Indels 2; Gaps 1;

QY 3143 TTTGTTGCCATTTAAATTTCTGTTCCCTCTAGCTTAGTAATTTTAGGATTTTAAATAACA 3202
Db 47 TTTTTCCTTTTTCGCTTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 106
QY 3203 ACTATTGAAATCATGACATACGTTTAAATGATATTTTAAATACGTTAGGCTATAAACC 3262
Db 107 CTTTATAATTAAGAAAAAATTTTAAAGTTTATTTTCCAGCACCACTTGAATTAATAC 166
QY 3263 TTTTAAATTTTTTAAAAAATAAGATGAGTGTGGCTCATGCTGTAAATCCCAACTT 3322
Db 167 TGAATAAATTAACATAAATGAGGCTGGTATAGTGGCTTATGCTATAATATCCAGCACTT 226
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QY 3323 TGGAGAGCCGGTCCGGAGGATAGCTTGATCCAGCAGTTCAGACCAGTCAGGGCAACA 3382
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
227 TGGAGAGCCGGTCCGGAGGATAGCTTGATCCAGCAGTTCAGACCAGTCAGGGTGAACA 286
QY 3383 CAGCAAGACCCCATATCTTAAAAAACAACAAACAAAATACCTGGGTATGGTTGTGC 3442
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
287 TAGTGAGATCTGTCTGCAAAAAAATAATGTTTAAATCAGCAGGTGGTGTGC 346
QY 3443 TCACCTGTAGTCCAGCTACACAGGAGCTGAGGCGAGAGGATCATCTTGAGCCAGGAGG 3502
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
347 CTGCTGTAGTTTCAGATATCTCAGAGGCTAAGGTGGAAGGATGCTTCAGTCCAGGAGT 406
QY 3503 TTGAGGCTCGAGTGCATGATGACGCGCTGCTACACT--CAGTCTGGGTGACAGTCAAG 3560
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
407 TTGAGGCTCGAGTGAAGCTATGATCATGTCATTCAGCTTCAGCTTTGGGTGACAGAGCAAG 466
QY 3561 AAGCTGTCTCAAAAAATAATAATAAAAAATAACTTTTAAAAACAACAAAATTAATTA 3620
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
467 ACCCTGTCTCAACAAAACACAGAGTATGTATATGATATATAGTCCAGGTATTATTTA 526
QY 3621 ATTTTAAAA 3629
Db |||||
527 ACAGTAATA 535

RESULT 13
US-09-949-016-12256/c
; Sequence 12256, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12256
; LENGTH: 36228
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12256
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Query Match 3.2%; Score 182.8; DB 4; Length 36228;
Best Local Similarity 62.4%; Pred. No. 7.9e-32;
Matches 322; Conservative 0; Mismatches 187; Indels 7; Gaps 2;

QY 3195 AAATAACAACCTATTGAAATCATGACATACGTTTAAATGATATATTATTAACGTTAGGC 3254
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
7176 ACACAACAACAACAAAAAGATAAATCTGACCTTTATTAAAGTTAAAACTTGAACCTTCAA 7117
QY 3255 TATAAACCTTTTAAATTTTTTAAAAAATAGATGATGTTGGTCTCATGCTGTAATCC 3314
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
7116 AGATACCATAGAATAATGAATAAGGAGCCAGGTCAGTGGCTCAGCCTGTAATCC 7057
QY 3315 CAACACTTTGGGAAGCCGGGTCCGGAGGATAGCTTTGAGTCAGCAGATTTTGAGACCAGTCA 3374
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
7056 CACCACCTTTGGAGCCGAGCGGGGGATTCCTTTGAGCCAGGAGTTCGAGACCAGTCT 6997
QY 3375 GGGCAACACAGCAACCCCATATCTAAAAAACAACAAAACAAAATTAACCTGGGTAT 3434
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
7116 AGATACCATAGAATAATGAATAAGGAGCCAGGTCAGTGGCTCAGCCTGTAATCC 7057
QY 3315 CAACACTTTGGGAAGCCGGGTCCGGAGGATAGCTTTGAGTCAGCAGATTTTGAGACCAGTCA 3374
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
7056 CACCACCTTTGGAGCCGAGCGGGGGATTCCTTTGAGCCAGGAGTTCGAGACCAGTCT 6997
QY 3375 GGGCAACACAGCAACCCCATATCTAAAAAACAACAAAACAAAATTAACCTGGGTAT 3434
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
6996 GGCCAACATGGCAAAACCCCTGCTCT-----ACTAAAAATACAAAAATTAGCCTGGGT 6943
QY 3435 GGTGTGCTCACCCTGATGTCAGGATACACAGGAAGCTGAGGCAGAGGATCAGCTTGAGC 3494
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
6942 GGTGGGGGCACCTGTATCCAGTTACTCAGGAGGCTGAGGAGGAGTTCGTTGAGC 6883
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QY 3495 CCAGGAGTTGAGGTCAGTGCATGATCCATGAACGCGCTGCTACACT-CAGTCTGGGTGACA 3553
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
6882 CCGGAGGCGAGAGGTTGCAGTGAGCAAGATCAGCGCGTTGCACCTCCAGCAGGCGACA 6823
QY 3554 GTGCAAGAAGCTGCTCAAAAAATAATAATAATAATAATACTTTTAAAAAACAACAAAT 3613
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
6822 GAGCAAAATCTCATCTCAAAAAAATAATAATAATAATAATAATAATAATAATAATAATA 6763
QY 3614 TAATTAATTTTAAAAACACACACACATAGATGTTTGCATAATTCGATTAAGGACCTGTATCTAGAA 3673
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
6762 TCATGAATAGGATAAATAATTTTGCATAATTCGATTAAGGACCTGTATCTAGAA 6703
QY 3674 TATATCCCTGGAGTTAAATTTTAAAAATATTTAGAAGA 3709
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
6702 TATAAAAAGAAATCTTGTAACTCAATAATAAGAAGA 6667

RESULT 14
US-09-949-016-15468/c
; Sequence 15468, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15468
; LENGTH: 36228
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15468

Query Match 3.2%; Score 182.8; DB 4; Length 36228;
Best Local Similarity 62.4%; Pred. No. 7.9e-32;
Matches 322; Conservative 0; Mismatches 187; Indels 7; Gaps 2;

QY 3195 AAATAACAACCTATTGAAATCATGACATACGTTTAAATGATATATTATTAACGTTAGGC 3254
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
7176 ACACAACAACAACAAAAAGATAAATCTGACCTTTATTAAAGTTAAAACTTGAACCTTCAA 7117
QY 3255 TATAAACCTTTTAAATTTTTTAAAAAATAGATGATGTTGGTCTCATGCTGTAATCC 3314
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
7116 AGATACCATAGAATAATGAATAAGGAGCCAGGTCAGTGGCTCAGCCTGTAATCC 7057
QY 3315 CAACACTTTGGGAAGCCGGGTCCGGAGGATAGCTTTGAGTCAGCAGATTTTGAGACCAGTCA 3374
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
7056 CACCACCTTTGGAGCCGAGCGGGGGATTCCTTTGAGCCAGGAGTTCGAGACCAGTCT 6997
QY 3375 GGGCAACACAGCAACCCCATATCTAAAAAACAACAAAACAAAATTAACCTGGGTAT 3434
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
6996 GGCCAACATGGCAAAACCCCTGCTCT-----ACTAAAAATACAAAAATTAGCCTGGGT 6943
QY 3435 GGTGTGCTCACCCTGATGTCAGGATACACAGGAAGCTGAGGCAGAGGATCAGCTTGAGC 3494
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
6942 GGTGGGGGCACCTGTATCCAGTTACTCAGGAGGCTGAGGAGGAGTTCGTTGAGC 6883
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Db 6822 GAGCAAACTCCATCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAAAAATGAAAAAGACAAC 6763
Qy 3614 TAATTAATTTTAAAAACACACACACTAGATGCTTTGCAATTTGATTTATTTGGGAGTC 3673
Db 6762 TCAATGAATAGGATAAATAATTTGCAATCATATATCTGATAAGGACCTGTATCTAGAA 6703
Qy 3674 TATATCCCTGGAAGTTAATTTAAAAATATTTAGAAGA 3709
Db 6702 TATAAAGAATCTTGTAACTCAATAATAGAAGA 6667

RESULT 15
US-09-949-016-12672/c
; Sequence 12672, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12672
; LENGTH: 134140
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(134140)
; OTHER INFORMATION: n = A, T, C or G
US-09-949-016-12672

Query Match 3.2%; Score 182.6; DB 4; Length 134140;
Best Local Similarity 64.4%; Pred. No. 1.5e-31;
Matches 289; Conservative 0; Mismatches 159; Indels 1; Gaps 1;
Qy 3268 AATTTTAAAAAATAGATGAGTGGTGGCTCATGCTTAATCCCAACACTTTGGGA 3327
Db 94152 AAAATGTACAAGAAATATATGCGCGGTGTAGTGTGCTGTAAATCCAGCACTTAGGA 94093
Qy 3328 AGCGGGTGGGAGGATAGCTTCCAGCAGTGTGAGACCACTGAGGGCAACACAGCA 3387
Db 94092 AGCAAGATGGGAGTATCACTTAAGCCAGGAGTTCAGGATCAGCCTAGACACATGGAG 94033
Qy 3388 AGACCCCATATCTAAAAAACAACAAACAAATACCTGGGTATGGTTGCTCACC 3447
Db 94032 AATCCTCTCTACAAAAACAAAAAATACAAAAATTTAGCTGGGTGTGATGGTACACGCC 93973
Qy 3448 TGTAGTCCAGCTACACAGGAAGCTGAGGAGGATCACTTGAGCCAGGAGTTGAG 3507
Db 93972 TGTAGTCCAGCTACAGGAGTGAAGTGGGAGGATCACTTGAGCCAGGAGTTGAG 93913
Qy 3508 GCTGCACTGATCCATGAACCGCTGCTACACTC-AGTCTGGGTGACAGTCAAGAGCTG 3566
Db 93912 ACTGCACTGATCCATGATTGTGCCACTGCACTTAGCCTTTGGTGACACAATAAGACCTG 93853
Qy 3567 TCTCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3626
Db 93852 TTTCCAAAAAGAAAGAAAGAAAGAAAGAAATTTTCACTATGAGTGAATAT 93793
Qy 3627 AAACACACACACTAGATGTTTCAATTTGATTTTGGGAGTCTATATCCTCGAA 3686
Db 93792 TAGACACACACAACTTTAACTGATGAGATTGTAGGAGATAAATAATGTTGAGTTAAA 93733
Qy 3687 GTTAATTTAAAAATATTTAGAGAGTCTT 3715

Db 93732 TAAAAATTAATTCAGAAAGGAAAAATTTGTTT 93704
Search completed: November 1, 2005, 20:13:12
Job time : 857 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 1, 2005, 19:18:42 ; Search time 4062 Seconds
(without alignments)
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Title: US-10-030-294-1
Perfect score: 5676
Sequence: 1 cagctgttcaggatgctcg.....tttataattgttccctcgt 5676

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9784742 seqs, 4129495052 residues

Total number of hits satisfying chosen parameters: 19569484

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
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25: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*
26: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
27: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
28: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	632.6	11.1	633	13	US-09-925-065A-842014
C 2	196.2	3.5	65793	22	Sequence 842014, Sequence 3, Appli
C 3	196	3.5	304905	19	Sequence 1, Appli
4	193.8	3.4	536	13	US-10-271-416-1
5	193	3.4	13070	22	US-09-925-065A-552295
					Sequence 17605, A

C	6	193	3.4	156318	22	US-10-741-600-17574	Sequence 17574, A
C	7	192.2	3.4	536	13	US-09-925-065A-552294	Sequence 552294, A
C	8	188.4	3.3	135005	21	US-10-723-860-2320	Sequence 2320, Ap
C	9	188.4	3.3	135005	24	US-10-756-149-1719	Sequence 1719, Ap
C	10	187.6	3.3	8133	19	US-10-380-124-10	Sequence 10, Appl
C	11	186	3.3	587	13	US-09-925-065A-123687	Sequence 123687, A
C	12	186	3.3	18861	11	US-09-984-423-513	Sequence 513, App
C	13	185.6	3.3	606	13	US-09-925-065A-901413	Sequence 901413, A
C	14	185.6	3.3	610	13	US-09-925-065A-907871	Sequence 907871, A
C	15	185.6	3.3	611	14	US-10-027-633-181221	Sequence 181221, A
C	16	185.6	3.3	611	18	US-10-027-633-181221	Sequence 181221, A
C	17	185.4	3.3	3287	14	US-10-027-633-115440	Sequence 115440, A
C	18	185.4	3.3	3287	18	US-10-027-633-115440	Sequence 115440, A
C	19	185.4	3.3	47999	24	US-10-477-729A-4	Sequence 4, Appli
C	20	184.4	3.2	587	13	US-09-925-065A-123685	Sequence 123685, A
C	21	184.4	3.2	587	13	US-09-925-065A-123686	Sequence 123686, A
C	22	183	3.2	335199	22	US-10-496-011-4	Sequence 4, Appli
C	23	182.6	3.2	615	13	US-09-925-065A-916797	Sequence 916797, A
C	24	182.6	3.2	47903	20	US-10-322-281-808	Sequence 808, App
C	25	182.4	3.2	736	14	US-10-027-633-17813	Sequence 17813, A
C	26	182.4	3.2	736	18	US-10-027-633-17813	Sequence 17813, A
C	27	182.2	3.2	36651	9	US-09-964-469-3	Sequence 3, Appli
C	28	182.2	3.2	36651	17	US-10-425-962-3	Sequence 3, Appli
C	29	182	3.2	570	13	US-09-925-065A-517201	Sequence 517201, A
C	30	182	3.2	570	13	US-09-925-065A-517202	Sequence 517202, A
C	31	182	3.2	55735	22	US-10-741-600-17698	Sequence 17698, A
C	32	181.8	3.2	728	13	US-09-925-065A-918286	Sequence 918286, A
C	33	181.8	3.2	728	13	US-09-925-065A-918287	Sequence 918287, A
C	34	181.8	3.2	50000	18	US-10-364-505-8	Sequence 8, Appli
C	35	181.8	3.2	50000	20	US-10-681-199-8	Sequence 8, Appli
C	36	181.4	3.2	728	13	US-09-925-065A-918288	Sequence 918288, A
C	37	181.4	3.2	45806	21	US-10-719-993-6943	Sequence 6943, Ap
C	38	181.2	3.2	113589	24	US-10-764-425-9	Sequence 9, Appli
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C	41	181	3.2	693	13	US-09-925-065A-709225	Sequence 709225, A
C	42	181	3.2	693	13	US-09-925-065A-709226	Sequence 709226, A
C	43	181	3.2	693	13	US-09-925-065A-709227	Sequence 709227, A
C	44	181	3.2	58985	10	US-09-901-152-3	Sequence 3, Appli
C	45	181	3.2	58985	22	US-10-483-593-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-925-065A-842014
; Sequence 842014, Application US/0925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108927.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 842014
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Homo sapiens
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Db	155885	CTACAAAAAATAATACAAAAACGTTAGCCAGGTGTGGTGGTGCAAAACCTGTAGTTTTCAG	155826	
QY	3459	CTACACAGGAAGCTCAGGCAGAGGATCACTTGAAGCCAGGAGGTTGAGGCTGCAGTGTAT	3518	
Db	155825	CTGCTCAGAGGCTCAGGTGGGAGGATCACTTGAAGCCAGGAGGTTGAGGCTGCAGTGTAT	155766	
QY	3519	CCATGAACGCGCTGCTTACACT--CAGTCTGGGTGACAGTGCAGAGAGCTGTCTCAAAAAATA	3577	
Db	155765	TCGTGATCGCGCACTGCACCTCCAGCTGGGTGACAGAGTAAGACCCCGTCTCAAAAAA	155706	
QY	3578	ATAAATAAATAAAAAATACTTTTAAAAACAAAAATTAATTAATTTTAAAAACACAACA	3637	
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; Sequence 552295, Application US/09925065A				
; Publication No. US2005028172A9				
; GENERAL INFORMATION:				
; APPLICANT: Wang, David G.				
; TITLE OF INVENTION: Identification and Mapping of Single				
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome				
; FILE REFERENCE: 108827.135				
; CURRENT APPLICATION NUMBER: US/09/925,065A				
; CURRENT FILING DATE: 2001-08-08				
; PRIOR APPLICATION NUMBER: US 60/243,096				
; PRIOR FILING DATE: 2000-10-24				
; PRIOR APPLICATION NUMBER: US 60/252,147				
; PRIOR FILING DATE: 2000-11-20				
; PRIOR APPLICATION NUMBER: US 60/250,092				
; PRIOR FILING DATE: 2000-11-30				
; PRIOR APPLICATION NUMBER: US 60/261,766				
; PRIOR FILING DATE: 2001-01-16				
; PRIOR APPLICATION NUMBER: US 60/289,846				
; PRIOR FILING DATE: 2001-05-09				
; NUMBER OF SEQ ID NOS: 957086				
; SOFTWARE: FastSeq for Windows Version 4.0				
; SEQ ID NO 552295				
; LENGTH: 536				
; TYPE: DNA				
; ORGANISM: Homo sapiens				
US-09-925-065A-552295				
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Best Local Similarity 70.9%; Pred. No. 1.6e-30;				
Matches 270; Conservative 1; Mismatches 108; Indels 2; Gaps 1;				
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Db	1	ATCTGTACAAAACATCTGATTTTCAAAAATCTTTAGTAGTAGTAAGTTAAATCTTA	60	
QY	3272	TTTTAAAAAATAGATGAGTGTGGTGGCTATGCTGTAAATCCCAACACTTTTGGGAAGCC	3331	
Db	61	AAAGTCAAAGATTGCTGGGTATGGTAGCTCACGCTGTAAATTTCAACACTCTAGGAGCC	120	
QY	3332	GGGTGGGAGGATAGCTTGAAGTCCAGAGTGTGAGACAGTCCAGGCGCAACAGCAAGAC	3391	
Db	121	GAGGGGGGGCTATCGTTGAGCCAGGGGTTTGAACACAGCTAGGGCAACAGGCAAAAC	180	
QY	3392	CCCATATCTTAAAAAACAACAAAAAATACTGGGTATGGTTGTGCTCAGCTCTGTA	3451	
Db	181	CCCATCTCTTACAAAATAAAAATACA--ATAATGAGCTGGGCATGGTGCCACCACTGTG	238	
QY	3452	GTCCAAGCTTACACAGGAAGCTCAGGCGAAGGATCACTTGAAGCCAGGAGGTTGAGGCTG	3511	
Db	239	GTCCCAGCTACTTGGGAGGCTGAGCGAGAGATGGCTTGAGCCCAAGGAKGTTGGGCTG	298	
QY	3512	CAGTGATCCATGAACCGCGCTGTACACTCAGTCTGGGTGACAGTGCAGAGCTGTCTCA	3571	

Db 299 CAGTGCAGCTGTGACTGTACTACTGCACCTCCACCTAGGTGACAGAAATAAGACCCCTGTCTCA 358
 Qy 3572 AAAATAATAATAATAATAAAAA 3592
 Db 359 AAAATAAACAAATAAAAAATAA 379
 RESULT 5
 US-10-741-600-17605
 ; Sequence 17605, Application US/10741600
 ; Publication No. US20050026169A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele et al.
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; FILE REFERENCE: CL001499
 ; CURRENT APPLICATION NUMBER: US/10/741.600
 ; CURRENT FILING DATE: 2003-12-22
 ; NUMBER OF SEQ ID NOS: 73997
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 17605
 ; LENGTH: 13070
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-741-600-17605
 Query Match 3.4%; Score 193; DB 22; Length 13070;
 Best Local Similarity 70.8%; Pred. No. 1.1e-29;
 Matches 271; Conservative 0; Mismatches 110; Indels 2; Gaps 1;
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 Db 10423 ATATCTGTACAAAACATCTGATTTTCACCTTTTCAAAATCTTTAGGTAGTAAAGTTAAAAATC 10482
 Qy 3270 TTTTAAAAAAATAGATGAGTGTGGCTCATGCGCTGTAATCCCAACACATTTTCGGGAAG 3329
 Db 10483 TAAAGGTCAAGATGTCTGGGTATGGTAGCTCAGCCCTGTAAATCCAAACATCTTAGGAGG 10542
 Qy 3330 CCGGGTCGGGAGGATAGCTTTGAGTCCAGCAGTGTGAGACCAAGTTCAGGGCAACACAGCAAG 3389
 Db 10543 CCGAGGCGGCATATCGCTTGAGCCAGGGGTGTTGAGACCAGCTAGGGCAACAGGCAAA 10602
 Qy 3390 ACCCATATCTAAAAAACAACAAACAAATAATTTACCTGGGTATGGTTGTGCTCACCTG 3449
 Db 10603 ACCCATCTCTACAAAAATAAAATACAA--ATAATGAGCTGGGCATGGTGGCAGCACCTG 10660
 Qy 3450 TAGTCCAGCTACACAGGAAGCTCAGCAGAGAGGATCACTTGAGCCAGGAGTTTGAGGC 3509
 Db 10661 TGGTCCCAAGCTACTTGGGAGGCTGAGGAGGAGGATGGCTTGAGCCAGGAGGTTTGGGGC 10720
 Qy 3510 TGCACTGATCCATGAACCGCTGCTACACTCAGTCTGGGTGACAGTGCAGAGAGCTGTCT 3569
 Db 10721 TGCACTGAGCTGTGACTGTACTCTGCACTCCACCTAGTGCACAGAATAAGACCCCTGTCT 10780
 Qy 3570 CAAAAATAATAATAATAAAAA 3592
 Db 10781 CAAAAATAAACAAATAAAAAATAA 10803
 RESULT 6
 US-10-741-600-17574/c
 ; Sequence 17574, Application US/10741600
 ; Publication No. US20050026169A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele et al.
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; FILE REFERENCE: CL001499
 ; CURRENT APPLICATION NUMBER: US/10/741.600
 ; CURRENT FILING DATE: 2003-12-22
 ; NUMBER OF SEQ ID NOS: 73997
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 17574

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: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CLO01499
: CURRENT APPLICATION NUMBER: US/10/741.600
: CURRENT FILING DATE: 2003-12-22
: NUMBER OF SEQ ID NOS: 73997
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 17574

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; LENGTH: 156318
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(156318)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-17574

Query Match          3.4%; Score 193; DB 22; Length 156318;
Best Local Similarity 70.8%; Pred. No. 4e-29;
Matches 271; Conservative 0; Mismatches 110; Indels 2; Gaps 1;

QY 3210 AAATCATGACATACGTTTAAATGATATTTTAAATACGTTAGGCTTATAACCTTTTAAA 3269
Db 66635 ATATCTGTACAAACAATCTGATTTCACTTTTCAAAATCTTTAGTAGTAAAGTTAAATC 66576

QY 3270 TTTTAAATAAATAGATGAGTGTGGTGTCTATGCTGTAAATCCCAACACTTTGGGAAG 3329
Db 66575 TAAAGGTCAAAGATTGCTGGGTATGGTAGCTACGCTGTAAATCCCAACACTTAGGAGG 66516

QY 3330 CCGGTCGGGAGGATAGCTTGACTCCAGCAGTTTGAGACCAGTCAGGGCAACACACAAG 3389
Db 66515 CCGAGCGGCGCATATCGCTTGAGCCCGAGGGGTTTGAGACAGTAGTGGGCAACAGCAAA 66456

QY 3390 ACCCCATATCTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3449
Db 66455 ACCCATCTCTACAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 66398

QY 3450 TAGTCAAGCTACACAGGAAGCTGAGGCAAGAGATCACTTGAGCCAGGAGGTTGAGGC 3509
Db 66397 TGGTCCAGCTACTTGGAGGCTGAGGAGGAGGATGGCTTGAGCCAGGAGGTTGGGC 66338

QY 3510 TCGAGTGATCCATGACGCGCTGCTACACTCAGTCTGGGTGACAGTGCAGAGCTGTCT 3569
Db 66337 TGCAGTGAGCTGAGCTGACTACTGCTACTGCTCCACTCCACTAGGTGACAGAAATAGACCCCTGTCT 66278

QY 3570 CAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3592
Db 66277 CAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 66255

RESULT 7
US-09-925-065A-552294
; Sequence 552294, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 552294
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-552294

Query Match          3.4%; Score 192.2; DB 13; Length 536;
Best Local Similarity 70.6%; Pred. No. 3.4e-30;
Matches 269; Conservative 1; Mismatches 109; Indels 2; Gaps 1;

QY 3212 ATCATGACATACGTTTAAATGATATTTTAAATACGTTAGGCTATAAACCTTTTAAAT 3271
Db 1 ATCTGTACAAACAATCTGATTTTCACTTTTCAAAATCTTTTAGTAGTAAAGTTAAATCTTA 60

QY 3272 TTTTAAAAAATAGATGAGTGTGGTGTCTATGCTGTAAATCCCAACACTTTGGGAAGCC 3331
Db 61 AAGGTCAAAGATTGCTGGGTATGGTAGCTACGCTGTAAATCCCAACACTCTAGGAGGCC 120

QY 3332 GGGTCGGGAGGATAGCTTGAGTCCAGCAGTTTGAGACCAAGTCAGGCGCAACACAGCAAGAC 3391
Db 121 GAGGGGGGRTATCGCTTGAGCCCGAGGGGTTTGAGACCAGCTAGGCGCAACAAAGGCAAAAC 180

QY 3392 CCCATATCTTAAAAAACAACAAACAAAAATTTACTGGGTATGGTGTGCTCACCTGTA 3451
Db 181 CCATCTCTACAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 238

QY 3452 GTCCAAGCTTACACAGGAAGCTGAGGCAGAAAGATCACTTTGAGCCCGAGGAGGTTGAGGCTG 3511
Db 239 GTCCAGCTACTTGGGAGGCTGAGGCAGGAGGATGGCTTGAGCCCGAGGATGTTGGGCTG 298

QY 3512 CAGTGATCATGAACGCGCTGCTACACTCAGTCTGGGTGACAGTGCAGAAAGCTGTCTCA 3571
Db 299 CAGTGAGCTGTGACTGTACTACTGCACTCCACTAGGTGACAGAAATAAGACCTGTCTCA 358

QY 3572 AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3592
Db 359 AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 379

RESULT 8
US-10-723-860-2320
; Sequence 2320, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2320
; LENGTH: 135005
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-2320

Query Match          3.3%; Score 188.4; DB 21; Length 135005;
Best Local Similarity 71.8%; Pred. No. 3.5e-28;
Matches 260; Conservative 0; Mismatches 101; Indels 1; Gaps 1;

QY 3263 TTTTAAATTTTAAAAAATAAGATGAGTGTGGTGTCTCATGCTGTATATCCCAACACTT 3322
Db 26435 TTTTAAAAATGGTGACAGTGGCTGAGTGCAGTGGCTCATGCTGTATATCCCAACACTT 26494

QY 3323 TGGGAAGCGGTCGGGAGGATAGCTTGAGTCCAGCAGTGTTCAGACCACTCAGGGCAACA 3382
Db 26495 TGGGAGGCTGAGGAGGGGATGCTTGAGCCCATAGTTTGAGACCACCTTGGCCCAACA 26554

QY 3383 CAGCAAGACCCCATATCTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3442
Db 26555 GGGTAAATCCCATCTCAACAAAAATAACACACAAAAAATTAGCTGGGCATGGTGTGT 26614

QY 3443 TCACCTGTAGTCCAGCTACACAGGAAGCTGAGGAGGATCACTTTCAGCCAGGAGG 3502
Db 26615 ACATCTGTGTCCAGCTACTCAGGAGGCCGAGGTGGGAGGATCACTTTCAGCCAGGAGG 26674
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; LENGTH: 156318
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(156318)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-17574

Query Match          3.4%; Score 193; DB 22; Length 156318;
Best Local Similarity 70.8%; Pred. No. 4e-29;
Matches 271; Conservative 0; Mismatches 110; Indels 2; Gaps 1;

QY 3210 AAATCATGACATACGTTTAAATGATATTTTAAATACGTTAGGCTTATAACCTTTTAAA 3269
Db 66635 ATATCTGTACAAACAATCTGATTTCACTTTTCAAAATCTTTAGTAGTAAAGTTAAATC 66576

QY 3270 TTTTAAATAAATAGATGAGTGTGGTGTCTATGCTGTAAATCCCAACACTTTGGGAAG 3329
Db 66575 TAAAGGTCAAAGATTGCTGGGTATGGTAGCTACGCTGTAAATCCCAACACTTAGGAGG 66516

QY 3330 CCGGTCGGGAGGATAGCTTGACTCCAGCAGTTTGAGACCAGTCAGGGCAACACACAAG 3389
Db 66515 CCGAGCGGCGCATATCGCTTGAGCCCGAGGGGTTTGAGACAGTAGTGGGCAACAGCAAA 66456

QY 3390 ACCCCATATCTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3449
Db 66455 ACCCATCTCTACAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 66398

QY 3450 TAGTCAAGCTACACAGGAAGCTGAGGCAAGAGATCACTTGAGCCAGGAGGTTGAGGC 3509
Db 66397 TGGTCCAGCTACTTGGAGGCTGAGGAGGAGGATGGCTTGAGCCAGGAGGTTGGGC 66338

QY 3510 TCGAGTGATCCATGACGCGCTGCTACACTCAGTCTGGGTGACAGTGCAGAGCTGTCT 3569
Db 66337 TGCAGTGAGCTGAGCTGACTACTGCTACTGCTCCACTCCACTAGGTGACAGAAATAGACCCCTGTCT 66278

QY 3570 CAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3592
Db 66277 CAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 66255

RESULT 7
US-09-925-065A-552294
; Sequence 552294, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 552294
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-552294

Query Match          3.4%; Score 192.2; DB 13; Length 536;
Best Local Similarity 70.6%; Pred. No. 3.4e-30;
Matches 269; Conservative 1; Mismatches 109; Indels 2; Gaps 1;

QY 3212 ATCATGACATACGTTTAAATGATATTTTAAATACGTTAGGCTATAAACCTTTTAAAT 3271
Db 1 ATCTGTACAAACAATCTGATTTTCACTTTTCAAAATCTTTTAGTAGTAAAGTTAAATCTTA 60

QY 3272 TTTTAAAAAATAGATGAGTGTGGTGTCTATGCTGTAAATCCCAACACTTTGGGAAGCC 3331
Db 61 AAGGTCAAAGATTGCTGGGTATGGTAGCTACGCTGTAAATCCCAACACTCTAGGAGGCC 120

QY 3332 GGGTCGGGAGGATAGCTTGAGTCCAGCAGTTTGAGACCAAGTCAGGCGCAACACAGCAAGAC 3391
Db 121 GAGGGGGGRTATCGCTTGAGCCCGAGGGGTTTGAGACCAGCTAGGCGCAACAAAGGCAAAAC 180

QY 3392 CCCATATCTTAAAAAACAACAAACAAAAATTTACTGGGTATGGTGTGCTCACCTGTA 3451
Db 181 CCATCTCTACAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 238

QY 3452 GTCCAAGCTTACACAGGAAGCTGAGGCAGAAAGATCACTTTGAGCCCGAGGAGGTTGAGGCTG 3511
Db 239 GTCCAGCTACTTGGGAGGCTGAGGCAGGAGGATGGCTTGAGCCCGAGGATGTTGGGCTG 298

QY 3512 CAGTGATCATGAACGCGCTGCTACACTCAGTCTGGGTGACAGTGCAGAAAGCTGTCTCA 3571
Db 299 CAGTGAGCTGTGACTGTACTACTGCACTCCACTAGGTGACAGAAATAAGACCTGTCTCA 358

QY 3572 AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3592
Db 359 AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 379

RESULT 8
US-10-723-860-2320
; Sequence 2320, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2320
; LENGTH: 135005
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-2320

Query Match          3.3%; Score 188.4; DB 21; Length 135005;
Best Local Similarity 71.8%; Pred. No. 3.5e-28;
Matches 260; Conservative 0; Mismatches 101; Indels 1; Gaps 1;

QY 3263 TTTTAAATTTTAAAAAATAAGATGAGTGTGGTGTCTCATGCTGTATATCCCAACACTT 3322
Db 26435 TTTTAAAAATGGTGACAGTGGCTGAGTGCAGTGGCTCATGCTGTATATCCCAACACTT 26494

QY 3323 TGGGAAGCGGTCGGGAGGATAGCTTGAGTCCAGCAGTGTTCAGACCACTCAGGGCAACA 3382
Db 26495 TGGGAGGCTGAGGAGGGGATGCTTGAGCCCATAGTTTGAGACCACCTTGGCCCAACA 26554

QY 3383 CAGCAAGACCCCATATCTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3442
Db 26555 GGGTAAATCCCATCTCAACAAAAATAACACACAAAAAATTAGCTGGGCATGGTGTGT 26614

QY 3443 TCACCTGTAGTCCAGCTACACAGGAAGCTGAGGAGGATCACTTTCAGCCAGGAGG 3502
Db 26615 ACATCTGTGTCCAGCTACTCAGGAGGCCGAGGTGGGAGGATCACTTTCAGCCAGGAGG 26674
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Matches	281;	Conservative	1;	Mismatches	116;	Indels	6;	Gaps	2;
QY	3195	AAATAACAACACTATTGAATCATGACATACATCGTTAAATGATATTAATTAATACATTAGGC	3254						
Db	546	AAATTAATAATATTACAAATCATACACAATAGATGTTGAGTTAAATTCNAATTCAGTTGAC	487						
QY	3255	TATAAACCTTTTAAATTTTAAATAAATAGAT-----GAGTGTGGTGGCTCATGCTGT	3309						
Db	486	TTTWTGATTTGGTATTTTAAATAAATAAAGTTGACCATGTGTGGTGGCTCGTGTCTGT	427						
QY	3310	AATCCCAACACTTTGGGAAGCGGTCGGGAGGATAGCTTGAGTCCAGCAGTTTGAGACC	3369						
Db	426	AATCCCAACACTTTGGGAAGCTTGAGTTGGAAGGATAGCTTGAGACCAGGAGTTTGAGACC	367						
QY	3370	AGTCAGGGCAACACAGCAAGACCCCATATCTAAATAAATAAATAAATAAATAAATAAATAA	3429						
Db	366	AGCCTGGCAACATGCGCAAGACCTCATCTCTACTAAAAATAAATAAATAAATAAATAA	307						
QY	3430	GGTATGTTGTGCTCACTCTAGTCCAGCTACACAGCAAGCTGAGGCAGAGGATCACT	3489						
Db	306	GGCATAGCAGTGTGTTCATATAGTCCAGCTACTCAGGAGGCACAGGTGGAGGATCGCT	247						
QY	3490	TGAGCCCAAGAGGTGAGGCTGCACTGATCCATGAACGCGCTGCTACACT-CAGTCTGGG	3548						
Db	246	TGAACCCAGGAGGTGAGGCTGCACTGATCAGCTGATCAGCACTCCAGCCTAGG	187						
QY	3549	TGACAGTCAAGAAGCTCTCTCAATAAATAAATAAATAAATAAATAAATAAATAAATAA	3592						
Db	186	TGACAGAGAAAGACCTTGTCTCAAGAAATAAGCAAAACAAATAAATAAATAAATAA	143						
RESULT 12									
US-09-984-429-513									
; Sequence 513, Application US/09984429									
; Publication No. US20040010132A1									
; GENERAL INFORMATION:									
; APPLICANT: Rosen et al.									
; TITLE OF INVENTION: 53 Human Secreted Proteins									
; FILE REFERENCE: P2018P2									
; CURRENT APPLICATION NUMBER: US/09/984,429									
; PRIOR FILING DATE: 2001-10-30									
; PRIOR APPLICATION NUMBER: 60/244,591									
; PRIOR FILING DATE: 2000-11-01									
; PRIOR APPLICATION NUMBER: 09/288,143									
; PRIOR FILING DATE: 1999-04-08									
; PRIOR APPLICATION NUMBER: PCT/US98/21142									
; PRIOR FILING DATE: 1998-10-08									
; PRIOR APPLICATION NUMBER: 60/061,463									
; PRIOR FILING DATE: 1997-10-09									
; PRIOR APPLICATION NUMBER: 60/061,529									
; PRIOR FILING DATE: 1997-10-09									
; PRIOR APPLICATION NUMBER: 60/071,498									
; PRIOR FILING DATE: 1997-10-09									
; PRIOR APPLICATION NUMBER: 60/061,527									
; PRIOR FILING DATE: 1997-10-09									
; PRIOR APPLICATION NUMBER: 60/061,536									
; PRIOR FILING DATE: 1997-10-09									
; PRIOR APPLICATION NUMBER: 60/061,532									
; PRIOR FILING DATE: 1997-10-09									
; NUMBER OF SEQ ID NOS: 727									
; SOFTWARE: PatentIn Ver. 2.0									
; SEQ ID NO 513									
; LENGTH: 18861									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
US-09-984-429-513									
Query Match									
Best Local Similarity									
Matches									
3.3%; Score 186; DB 11; Length 18861;									
Pred. No. 4.2e-28;									
Mismatches 0; Conservative 0; Indels 1; Gaps 1;									
QY	3265	TTAAATTTTAAATAAATAGATGAGTGTGGTGGCTCATGCTGTATCCCAACACTTTG	3324						

Db	5557	TAAAGTTGAAAAAATAATGACTAGTGCAGCGGCTCACAATGTCTAATCCAGCGCTTTG	5616						
QY	3325	GGAGCGGGTCGGGAGGATAGCTTTCAGTCCAGCAGTTTTCAGAGCCAGTTCAGGCAACACA	3384						
Db	5617	GGAGCGCGAGGTGGGAGAAATCACTTTCAGTCTCAGAGGTTTCAGAGCCAGCTTCAGCAACATA	5676						
QY	3385	GCAAGACCCCATATCTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	3444						
Db	5677	GCAAGACTTCATCTCTACTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	5736						
QY	3445	ACCTGTAGTCCAGCTACACAGGAGCTGAGGAGGAGGATCACTTCAGGCCAGGAGGTT	3504						
Db	5737	ACCTGTAGTCCAGCTACTCAGAAAGCTGAGGAGGAGGATCACTTCAGGAGGTT	5796						
QY	3505	GAGGCTCAGTGATCCATGAACGCGCTGCTACACT-CAGTCTGGGTGACAGTTCGAAGAAG	3563						
Db	5797	GAGGCTCAGTGATCCATGAACGCGCTGCTACACT-CAGTCTGGGTGACAGTTCGAAGAAG	5856						
QY	3564	CTGTCTCAAAAAATAATAA 3581							
Db	5857	CTGTCTCAAAAAAGACAAA 5874							
RESULT 13									
US-09-925-065A-901413/c									
; Sequence 901413, Application US/09925065A									
; Publication No. US20050228172A9									
; GENERAL INFORMATION:									
; APPLICANT: Wang, David G.									
; TITLE OF INVENTION: Identification and Mapping of Single									
; FILE REFERENCE: 108827.135									
; CURRENT APPLICATION NUMBER: US/09/925,065A									
; CURRENT FILING DATE: 2001-08-08									
; PRIOR APPLICATION NUMBER: US 60/243,096									
; PRIOR FILING DATE: 2000-10-24									
; PRIOR APPLICATION NUMBER: US 60/252,147									
; PRIOR FILING DATE: 2000-11-20									
; PRIOR APPLICATION NUMBER: US 60/250,092									
; PRIOR FILING DATE: 2000-11-30									
; PRIOR APPLICATION NUMBER: US 60/261,766									
; PRIOR FILING DATE: 2001-01-16									
; PRIOR APPLICATION NUMBER: US 60/289,846									
; PRIOR FILING DATE: 2001-05-09									
; NUMBER OF SEQ ID NOS: 957086									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 901413									
; LENGTH: 606									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
US-09-925-065A-901413									
Query Match									
Best Local Similarity									
Matches									
3.3%; Score 185.6; DB 13; Length 606;									
Pred. No. 9.1e-29;									
Mismatches 272; Conservative 0; Mismatches 104; Indels 4; Gaps 2;									
QY	3251	AGGCTATAAACCTTTTAAATTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	3310						
Db	398	AGTTTTCATCTGTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	339						
QY	3311	ATCCCAACACTTTGGGAACCGGTCGGAGGATAGCTTTCAGTCCAGCAGTTTGAGACCA	3370						
Db	338	ATCCCAACACTTTGGGAACCGGTCGGAGGATAGCTTTCAGTCCAGCAGTTTGAGACCA	279						
QY	3371	GTCAGGGCAACACAGCAAGACCCCATATCT---AAAAAACAATAAATAAATAAATAAATAA	3427						
Db	278	GCCTGAACACATAGGAGACTCTGTCTACAAAAATAAATAAATAAATAAATAAATAAATAA	219						
QY	3428	TGGGTATGTTGTGCTCACCTGTAGTCCAGCTACAGAGCTGAGGAGGATCA	3487						
Db	218	TGGGGTGTGTCGCGAGCTGTAGTCCAGCTACTCAGAGGCTGAGGAGGATCA	159						
QY	3488	CTTGAGCCCAAGAGGTTGAGGCTGAGTGCATCATGAACGCGCTGCTACACT-CAGTCTG	3546						

Db 158 CTTGAGCCTGGGAGGTCAAGGCTGCAAGTGGCCGAGATTGCACCACTGCACCTCCAGCCTG 99
3547 GGTGACAGTCAAGAAGCTGCTCTCAAAATAATAATAATAATAATAATACTTTTAAAAAA 3606
Db 98 GGCTACAGAACCAGATCTCTCTCAAAAAAAGAAAGATGAAGGAAGAAAGAGACAATA 39
Qy 3607 CAAAAATTAATTAATTTTA 3626
Db 38 TAGATATGTTCCCTTTCTA 19

RESULT 14
US-09-925-065A-907871/c
; Sequence 907871, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 907871
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-907871

Query Match 3.3%; Score 185.6; DB 13; Length 610;
Best Local Similarity 71.6%; Pred. No. 9.1e-29;
Matches 272; Conservative 0; Mismatches 104; Indels 4; Gaps 2;

Qy 3251 AGCCTATAAACCTTTTAAATTTTAAAAAATAGATGAGTGGTGGCTCATGCCCTGTA 3310
Db 402 AGTTTTCACTGTTTAAAAAAGAAAAAAGGGGCTGACATGGTGGCTCATGCCCTGTA 343
Qy 3311 ATCCCAACACTTTTGGGAAGCCGGTCCGAGGATAGCTTGGTCCAGCACTTTTGAGACCA 3370
Db 342 ATCCAGCACTTTTGGGAGGCCAAGGAGGTGGATTGCTTGGAGCCAGGAGTTTGAGACCA 283
Qy 3371 GTCAGGGCAACAGCAGACCCCATATCT---AAAAAACAACAAACAAATTAAC 3427
Db 282 GCCTGAACACATAGGAGACTCTGTCTCTACAAAAAAGAAAAAAGAAAAATGGC 223
Qy 3428 TGGGTATGTTGCTCACCTGTAGTCCAGGATACACAGGAAGCTGAGGCAGAGGATCA 3487
Db 222 TGGGGTGGTGGTGGCGGCTGTAGTCCAGCTACTCTCAGGAGGCTGAGGCAGGAGGATCA 163
Qy 3488 CTTGAGCCCAAGGAGTTGAGGCTGCAGTGATCCATGAACCGCTGTCTACT-CAGTCTG 3546
Db 162 CTTGAGCCTGGAGGTCAAGGCTGCAGTGCAGCCGAGATTGCACCACTGCACCTCCAGCCTG 103
Qy 3547 GGTGACAGTCAAGAAGCTGCTCAAAATAATAATAATAATAATACTTTTAAAAAA 3606
Db 102 GGCTACAGAACCAAGTCTCTCTCAAAAAAAGAAATGAAGGAAGAAAGAGACAATA 43
Qy 3607 CAAAAATTAATTAATTTTA 3626
Db 42 TAGATATGTTCCCTTTCTA 23

RESULT 15
US-10-027-632-181221/c
; Sequence 181221, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 181221
; LENGTH: 611
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-181221

Query Match 3.3%; Score 185.6; DB 14; Length 611;
Best Local Similarity 71.6%; Pred. No. 9.1e-29;
Matches 272; Conservative 0; Mismatches 104; Indels 4; Gaps 2;

Qy 3251 AGCCTATAAACCTTTTAAATTTTAAAAAATAGATGAGTGGTGGCTCATGCCCTGTA 3310
Db 410 AGTTTTCACTGTTTAAAAAAGAAAAAAGGGGCTGAGCATGGTGGCTCATGCCCTGTA 351
Qy 3311 ATCCCAACACTTTTGGGAAGCCGGTCCGAGGATAGCTTGGTCCAGCACTTTTGAGACCA 3370
Db 350 ATCCAGCACTTTTGGGAGGCCAAGGAGGTGGATTGCTTGGAGCCAGGAGTTTGAGACCA 291
Qy 3371 GTCAGGGCAACAGCAGACCCCATATCT---AAAAAACAACAAACAAATTAAC 3427
Db 290 GCCTGAACACATAGGAGACTCTGTCTCTACAAAAAAGAAAAAAGAAAAATGGC 231
Qy 3428 TGGGTATGTTGCTCACCTGTAGTCCAGGATACACAGGAAGCTGAGGCAGAGGATCA 3487
Db 230 TGGGGTGGTGGTGGCGGCTGTAGTCCAGCTACTCTCAGGAGGCTCAGGCAGGAGGATCA 171
Qy 3488 CTTGAGCCCAAGGAGTTGAGGCTGCAGTGATCCATGAACCGCTGTCTACT-CAGTCTG 3546
Db 170 CTTGAGCCTGGAGGTCAAGGCTGCAGTGCAGCCGAGATTGCACCACTGCACCTCCAGCCTG 111
Qy 3547 GGTGACAGTCAAGAAGCTGCTCAAAATAATAATAATAATAATACTTTTAAAAAA 3606
Db 110 GGCTACAGAACCAAGTCTCTCTCAAAAAAAGAAATGAAGGAAGAAAGAGACAATA 51
Qy 3607 CAAAAATTAATTAATTTTA 3626
Db 50 TAGATATGTTCCCTTTCTA 31

Search completed: November 2, 2005, 04:52:20
Job time : 4073 secs

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